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Result
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Listing first 45 summaries
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No.	Score	Query Match	Length DB	. 8	D	Description
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J. Biol. Chem. 261:15455-15460(1986). [7] SEQUENCE OF 1-26. MEDIJNE=93184416; PubMed-8443384;	UENCE OF 19-37. LINE-87057168; PubMcd- dros E.V., Rothenberg : Ification andlecul	SEQUENCE FROM N.A. TISSUE-Bye; Strausberg R.; Stanitt-A (TYO 2000) to the EMPL Stank TDDBT databases.	 [4] SEPRINCE FROM N.A. SCALOR J., Johnson D., Angell S.; Sudedited (BIN 1998) for the EMELAD-RHALL/INDRI databases. [5] 	SEQUENCE FROM N.A. MEDLINE-95261033; PubMed 7742531; Regre A., Quadros E.V., Platica o., Mothenberg S.P.: "The calching and characterization of the human transcribation of open." gene." placed 95:2711-2714(1495).	[2] SECTION FERM N.A. SECTION FINAL NAME OF STATEMENT OF THE PROPERTY OF THE P	EXPLENCE FROM N.A. SEQUENCE FROM N.A. MEDILINE-91210-812; PubMed-1708394; History June Lko E., Quadros E.V., Regee A., Romain R., History S.P.; Rothenberg S.P.; "The cDNA sequence and the deduced amino acid sequence of human transcobalamin II show homology with rat intrinsic factor and human transcobalamin []; J. BIOL. Chem. 266:7860-7863(1991).	

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Best Local Similarity
Matches 374; Conserv
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Salvat G., Gueant J.,
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"Functional human transcobalamin II isoproteins are secreted by insect
cells asind the baculovirus expression system.":
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EMB.; BC001176; AAH01176.1; -.
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DISLARE SELECTEMY FRONTE IN VASTUES LEMS I ARLE
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SUBCELLULAR LOCATION: Secreted
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01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Transcobalamin II precursor (ICII) (FC II).
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                                                                                                                                                                                                                                                                                                                                                                                            EMBL.;
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-In FUNCTION: Primary vittmin Bl2-binding and transport protein.
-Delivers cobalamin to cells (by similarity).
-In SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                 EMBL; 80003720; MGD; MGI:98534;
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Mammalia; Eutheria; Rodentia; Sciuroquathi; Muridae; Murinae; Mus
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430 270

TRANSCOBALAMIN II.

InterPro; IPR002157; Cobalamin_bind.
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     modified and this statement is not removed outlines regulars a liberage appropriate (Sec.
                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL constation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its notion is in no way modified and this statement is not passed in the statement in the statement in the statement is not passed in the statement in the statement is not passed in the statement in the statement in the statement in the statement is not passed in the statement in the statement in the statement in the statement is not passed in the statement in the statement
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- FRUNCTION: Primary vitamin R12 binding and transport protein
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16-QCT-2001 (Rel. 40, Created)
16-QCT-2001 (Rel. 40, Last sequence update)
01:MAR 2002 (Rel. 41, Last annotation update)
Transcobalamin ii precursor (TCII) (TC II).
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TISSUE-Mammary gland, and Milk;
MEDLINE-99403038; Fithmed-1047-547;
Fodosav S.A., Bergland L., Hyzy E., (etersen T.E.)
"Serpense, S.S. bridges, and specific of bester track obtained expressed in Fichia pistoris.";
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Mammalia; Entheria; Cetarticdactyla; Euminantia; Pecera; Rovoldea;
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                                                                                                                                                                                                                                                SEQUENCE FROM N.A., PARTIAL SEQUENCE,
                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-9913;
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Best Local Similarity 63 0%;
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01-FEB-1991 (Rel. 17, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
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                                                                                                   10 VGLILESE-IPSQLICEICEVSE-ENYI------KLNPLLNIMIQSNYNRGTSAVNVVLSI, 61
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01-oCT-1996 (Ref. 34, Last sequence update)
01-MAR-2002 (Ref. 41, Last annotation update)
Intrinsic factor (revussor (IT) (INE) (Jastic Intrinsic factor):
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J. Biol. Chem. 268:2659-26579 (1973).
-1- PIRCTION: PROMOTES ABSTRICTION OF THE ESSENTIAL VITAMIN CORMINAL HORDON IN THE LEUM BY SPECIFIC RECEPTOR MEDIATED ENDOCYTOSIS.
-1- TISSUE SPECIFICITY: GASTRIC MICHOSA.
-1- SIMILARITY: RELOWIS TO THE EMPARYMENT CORMIAMIN TRANSPORT PROVEDING
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TISSUES STOMACH:
Historped M., Well M., Winnacker E.L.;
Hannaped M., Kehl M., Winnacker E.L.;
Submitted (Apr.1994) to the EMBL/GenBank/PDBJ databases.

FUNCTION: PROMOTES ABSONDTION OF THE ESSINTIAL VITAMIN COBALAMIN
CRE.) IN THE ILEUM BY SPECIFIC RECEPT & MIDIATED EMBORYFORIS.

-1- TISSUES EMBELIFICITY GASTRIC MUCOSA.
-1- TISSUES EMBOREMITAL PURNICIOUS ANEMIA SEEMS TO BE DUE TO DEFECT
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01-ADG-1992 (Rel. 23, Last sequence update)
01-MAP 2002 (Rel. 41, Last annotation update)
Intrinsic factor precursor (IF) (INF) (Vastric intrinsic factor).
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F27352;
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                                                                                                                                                                                                                                                                                                    Genomics 10:432-440(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                       SPOUENCE FROM N.A. MEDILINE 91301700; PubMed=2071148;
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between the Swiss Institute of Bioinformatics and the EMBL outstation
the European Bioinformatics Institute. There are no restrictions on it
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBIL; M63154; AAA66354.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to licensewisb-sib.ch).
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                                                                                                       PLLQGIADYRPKDGETI 369
                                                                                                                                         VSVKSGSVLLVVLEEAQPKNPMEKFETTMTSWG: VVSSINNIAENVNHKTYWQFLSGV-T
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                                                                                                                                                                       ISVLACSTVPHOVI KYABELCC-PTYETYASLSCHYLTSV--MCKAACEBEFWQLLEDINT
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                                                                                                                                                                                                                                                                                                           VYSTPLALQFLMTSPMRCAELGTACLKARVALLASLQDCAFQNALMISQLLPVLNHKTYI 251
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pOTENTIAL.
INTRINSIC FACTOR.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
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Pred. No. 1.7e-15;
Mismatches 155;
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Вb
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Best Local S
Matches 105
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MEDIINE-96105004: PubMed-7490275;
Maeda M., Asshara S., Nishi T., Mushiake S., Oka T., Shimada S.,
Maeda M., Asshara S., Nishi T., Mushiake S., Oka T., Shimada S.,
Chiba T., Tohyama M., Putai M.;
The rat intrinsic factor qene: its 5'-upstream region and chied
cell-specific transcription.";
J. Riochem. 117-1305-1311 (1945).

FUNCTION: PROMOTES ABSORPTION OF THE ESSENTIAL VITAMIN CHALAMIN
CUSL) IN THE ILEUM BY SEPCIFIC RECEPTOR-MEDIATED ENDACYTOSIS.

LITISSUE SPECIFICITY: GASTRIC MUCOSA.

FUNCTION: THE N-TERMINUS TO THE FUNAFYORIS CHARIN TPANSFULL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this Statement is not removed. Usage by and to common entitles requires a course agreement (see it) pressents of the house or send an email to licenses is both.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1990 (Rel. 15, Created)
01-OUT-1996 (Rel. 34, Last sequence update)
01-OUT-1996 (Rel. 34, Last annotation update)
01-MAR 2002 (Rel. 41, Last annotation update)
Intrinsic factor precursor (IF) (INF) (Gastric intrinsic factor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS EROY entry is repyriable. It is produced through a collaboration between the Swiss Institute of Bioinformation and the EMBL outstation the European Booinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01122; Cobalamin_bind;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-170 FROM N.A. SIKAIN=SPRAGUE-DAWLEY; TISSUE-Diver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIINE 88124816; PabMod-3422425;
Diockgraete B.K., Seetharam P., Banasrak L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Ra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IF_KAT
P17267; 035801;
                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                             САКВОНТЫ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rat gastric intrinsic factor.";
Proc. Nati. Acad. Sci. U.S.A. 85:46-50(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND SEQUENCE OF 262:276 AND 384-392
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56 SILIAMNLAS
                                  $ SIYVGLELSSIQAGTEEREYIHSI ELOVÇÇOLI OSAFSEH GEOGGERSMOZI ALYLI AL. 112
                                                                                                           ي
                                                                         YLLNVLWAVAGTSTRAQRSCSVPPDQQ
                                                                                                         FLLGVLGALT-----EMCETPEMDSHLVEKLGQHLLPWMDRLSL-------EHLNP-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JU3577; AAA41361.1; ALI_INTE
D45200; BAA08140.1; ALI_INITE
D45199; BAA08140.1; JUINED.
                                                                                                                                                                 Similarity
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19 117
19 417
26 246
103 288
143 182
209 209
311 311
330 330
413 413
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                                                                                                                                              Conservative
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                                                                                                                                                             14.68;
24.08;
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X
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· LYNLEAQKILITYQLMASDSADL · · ·
                                                                                                                                                               Score 263.5;
Pred. No. 3.
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RELINKED (GLONAC...) (POTENTIAL).

NELINKED (GLONAC...) (POTENTIAL).

NELINKED (GLONAC...) (POTENTIAL).

NELINKED (GLONAC...) (POTENTIAL).
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BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                Mismatches 152; Indels III; Gaps
                                                                                                                                                                                                                                          881BF5B2C77563C3 CRC64;
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                                                                     ----PWVNGLQLLMENSVTESDLPNP-55
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                                                                                                                                                                                  Length 417;
   *TNGQLALT IMAL
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                                Pram: PF01122; Gobalamin_bind; Pram: PF01122; Gobalamin_bind; T.
PR:SITE: PS09468; CHALAMIN_BINDING; L.
Lransport; Gobalt transport; Glycoprotein;
NON_TER

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                                                                                                                                                                                  the European Ricinformatics Institute. There are no institutions on use by non-profit institutions as long as its montest is in no modified and this statement is not removed. Usage by and for common entities reported a 15-25-3 groups (55-37); [3***, 1.3.5 %, 55-37] or send an email to licensedish-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haptocorrin precursor (R protein) (Cobalophilin) (Fragment). Sus scrofa (Plu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FIG. 1 BLOCKOM INVILED LANGUAGE.

-!- FUNCTION: MAY PLAY A RELE IN PERVENTING THE ARREST! H OF COBALAMIN ANALOGS PRODUCED BY BACTERIA, BINDS TO COBALAMIN ANALOGS GIOH AS CORTNAMIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hewitt J.E., Seetharam B., Teykam T.F., Alpres P.H.:
"Isolation and characterization of a cDNA encoding porcine gastric haptocorrin.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1990 (Pol 15 Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-MAR-2002 (Pol 4) Tast increation (Part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota: Motazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
Mammalia: Eutleria: Cetarticdaetyla; Suipa; Suidae; Sus.
                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWiss institute of Ricintermatics and the EMBL outstation -
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    CHAIN
                                                                                                                                  PIR: S09334; S09334.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 KADGIIGDIYSTGLAMQAISVTPEQPTK-EWIYCEKTMYTH KETKÇGKEGNPMSIAQILD 273
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                                                                                                                                                                                                                                                                                                                                                                             TISSUE SPECIFICITY: HAPTOCOKRINS ARE A FAMILY OF CORALAMIN BINDING GLYCOPROTEINS FOUND IN BLOOD, SALIVARY AND MUCUSAL SECRETIONS, PTM: CONTAINS AROUT 30% CAPROHYDRATES.
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                                                                                                                                                                                                                                                                                                                                                             SIMPLARITY: BELONGS TO THE EUKARYOTIC COBALAMIN TRANSPORT PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                       TO COBALAMIN ANALOGS SUCH AS COBINAMIDE. SURCELLULAR LOCATION: Secreted.
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NIGACO
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CARBOHYD
                                                                                                                                                    MEDILHE 99206606; FabMed 10192388; MEDILHE 99206606; FabMed 10192388; Kalman S., Misskell W., Haralbe B., Lammel G., Fan G., Hyman P.W., Olimper L., Grimwood J., Davis R.W., Stephens R.S.; "Comparative genomes of Chlamydia pheumobiae and G. trachomatis.")
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STRAIN=AK39; MEDLINE=20150255; PabMed=10684935

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22.4%; Pred. No. 0.14;
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85 IRON-SULFUR (POTENTIAL).
43993 MW; F893D50F7HC90062 CRC64;
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IRON-SULFUR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Skamrov A., Feoktistova E., Goldman M., Beabealashvilli R.; "Cloning and sequencing of Mycoplasma gallisepticum chromosome region containing operons $10 and rrn235."; submitted (ter-1947) to the FMELSTONERCREDITY TO 238 RIBOSOMAL KNA AND MAY -IF FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 238 RIBOSOMAL KNA AND MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interpro: IPR000597: Ribosomat_L3. pfam: pF00297: Ribosomat_Ls: 1. proLom: pD001374: Ribosomat_L5: 1. pRoSITE: PS00474: RIBOSOMAL_5: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycoplasma qallisepticum.
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15-per-1998 (kel. 37, Last sequence update)
30 MAY 2000 (kel. 39, Last annotation update)
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132 THEREAS FOR INTERESTRIBE VESTABLE DIRECTOR PROPERTY.
                                          174 TVF :
                                                                                                                           126 FLVSQLKWFLED---EKPAIDTAAMA-GLAFT-CLKRSNENPGRR------QRITMAIR 17
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                                                                                    PR KVSDLLK - VEELEGEGGVVDVGAKTKGKGFTGAIKFWNFKIGSKGHGAGYPHFFQGSVO 141
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hes 57; Conserv
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                                          FEITEAGTECHTCHECHTSTATISTIATIST ALS TATES AARCHECLALIGATIST. 751
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23.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-52880 / PY1679;
MEDLINE-97197971; Pubm
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Mol. Cert. Biol. 13.3541 3556(1943)
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Fukaryeta: Fundi Ascompenta: Saccharemycetica: Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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01-FEB-1994 (Rel. 28, Last sequence update)
16-0CT-2001 (Rel. 40, last annotation epdate
                                                                                                                                 REPEAU
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EMPL; Z72717, CAA96907.1; =
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coqlievina M., Klima R., Bertani I., Delneri D., Zaccaria P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
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SPISIONS CHARRED TRNA AND STIMULATING THE KINASE ACTIVITY OF COM2
IN AMINO ACTO STRANZED CELLS. REQUIRED IN VIVO FOR THE
PHOSPHORYLATION OF FIF-2-ALPHA ON SEPINE-52 BY THE PROTEIN KINASE
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PS50077; HEAT_REPEAT; 4
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 PubMed-9046087
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16-00T-2001 (Rel. 40, Created)
16-00T-2001 (Rel. 40, Last sequence update)
16-00T-2001 (Rel. 40, Last annotation update)
Scaling/Judick regramsporter (Hu(t),1()) outransporter) (Sudium-Todide
use by non-profit institutions as long modified and this statement is not removed.
                                                      between
                                                                                                                                                                                MEDLINE-96158880, PabMed 8559252;
Dai G., Levy O., Carrasco N.;
"Cloning and characterization of the thyroid iodide transporter.";
                                                                                                                                                                                                                                                                                                                                                                             symporter) (Nar/I:symporter).
SLC5A5 OR NIS.
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                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                      Nature 379:458-460(1996)
                                                                                                                                                                                                                                                                                                                      Eukaryota: Metasoa:
Mammalia. Eutheria,
                                 the European Bioinformatics Institute. There are no restrictions on
                                                                                                           -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS to THE SODIUM:SOLUTE SYMPORTER FAMILY (SSF).
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                         Raftus norvegicus (Rat.).
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    Mismathles 179, Indels 128,

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Pred. No.
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                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  980FDD03753E9D1C CRC64
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                                                                                  KESULT.
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| 16.407-2001 (Rol. 40, Created)
| 16.407-2001 (Rol. 40, Last sequence update)
| 16.407-2001 (Rol. 40, Last annotation update)
| Diaphanous protein boweled 4 (Diaphanous related formin 3) (DEF3)
                                                            NVWOH - VIO
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PRCSITE: PS00457: NA_SOLUT_SYMP_2: PALSE_NEG.
PRCSITE: PS50283: NA_SOLUT_SYMP_3: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.lsbrslb-ch/innonce, or send an email to license*isb-sib.ch).
                                                 QUNEV4;
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                                                                                                                                          80c. TALISALSOV - - - TASTSÖRAĞİ HSTI- - AÖLLAASTLEĞIĞĞI TAVASATIMARAV IQTAS
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                                                                                                                    CNTPGVLSGLAAG------LAVSLWVAVGATLYPPGEQTMGVLPTSAAGCTNDSVL 489
                                                                                                                                                                                        LMTSPMRGAEL--GTACLKARVALLASLÖDGAFQNALMISQLL--PVLNEKTYIDLIFPD 257
                                                                                                                                                                  I - - - SKGLSFTYGSACITY - AALSSLIGGGYLQGSFTYMGYTSGPILGAFT - LGMLLPA 439
                                                                                                                                                                                                               EDI POVPOLELAÇAY SOTI STASTSINAMAAVTV-EDI IKPRMPG------LAPRKI VE
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                                                                                                                                                                                                                                                                                                                                                                     618
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                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                           Fred. No. 2.5;
5. Mismatches
                                                                                                                                                                                                                                                                                                                    Score 93.5; DB
                                                                                                                                                                                                                                                                                                                                                                              PHOSPHORYLATION (BY CAPK) (POTENTIAL).
N-LINKED (GLONAC. . .) (FOTENTIAL).
N-LINKED (JENAI. . .) (FILEBITAL).
                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
CYTOPLASMIC (POTENTIAL)
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CYTOPLASMIC (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL)

POTENTIAL.
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EXTRACELLULAR (POTENTIAL)
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                                                            PRI;
                                                                                                                                                                                                                                                                                                                                                                     91EFAA6752B4F4B2 CRC64;
                                                            853 AA
                                                                                                                                                                                                                                                                                                                                  DB 1; Length 618;
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Mismatches 103; Indels

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Query Match
Best Local Similarity
Matches 52; Conserv
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ptam; PE02181; PH2; 1.
Pfam; PE02188; GoLoco; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- ALTERNATIVE PRODUCTS: 2 ISOSORMS: 1 (SHOWN HERE) AND 2: ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- DOMAIN: DEFS ARE RECULATED BY INTRAMOLECULAR GBD-DAD BINDING WHERE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Blum H., Bauersachs S., Mewes H.-W., Gassenhuber J., Wighthitted (JAN-2009) to the LMsL, Carbin, McEd databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Testis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
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DIAPH3 OR DIAP3
                                                                                                                                                                                                                                                                                                            DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMRL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003109; GoLoco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 468-853 FROM N.A. (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro: [PROGOGO4; Sec7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hateafia, 188033104, FH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: BINDS TO GIP-BOUND FORM OF RHO AND TO PROFILIN. ACTS IN A RHO-DEPENDENT MANNER TO RECKULT PROFILIN TO THE MEMBRANE. WHERE IT PROMOTES ACTIN POLYMERIZATION. IT IS REQUIRED FOR CYTOKINESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRESS FIBER FORMATION, AND TRANSCRIPTIONAL ACTIVATION OF THE SERUM RESPONSE FACTOR. DER PROTEINS COUPLE RHO AND SWI TYROSINE KINASE DURING SIGNALING AND THE REGULATION OF ACTIV DYNAMICS (F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RHO-GTP ACTIVATES THE DRES BY DISRUPTING THE GBD-DAD INTERACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL137718; CAH70890.1; ALI_INIT.
AL354829; CAC17664.1; ...
AL354829; CAC17665 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              coil; kepeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SM00498; FH2;
                                                                                                                            698
853 AA;
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                        4.8%;
23.5%;
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818
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                                                                                                                               MW.
                     Score 93; DB
Pred. No. 4.3;
                                                                                                                            IPNISE (IN ISOFORM 2).
MISSING (IN ISOFORM 2).
; B7FA9C745AE18CD9 CRC64.
                                                                                                                                                                                                                                                      COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
ARCZLYS-RICH (BASIC).
                                                                                                                                                                                                     VSVETLEKNIRGMGRGLGQLEKELETETETEDIHDKEVEKT -> GLCLEKKHEMALTESAKKLKTTPFTCMYFPLSHSVF
                                                                                                                                                                                                                                                                                                                                    COILED COIL (POIENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                             FH1 (PRO-RICH)
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                                                DB 1; Length 853;
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16-OCT-2001 (PAL 40, List sequence update)
16-OCT-2001 (PAL 40, List sequence update)
Mitogen-activated protein kinase 7 (EC 2.7.1.-) (Extracellular signal-regulated binase 5) (FEF-5) (BMKI binase).
    DOMAIN
                                                                                                      PROSITE: PS01351; MAPK: 1.

PROSITE: PS00107; PROTEIN_KINASE_ATP: 1.

PROSITE: PS00108: PROTEIN_KINASE_DOM: 1.

PROSITE: PS50011: PROTEIN_KINASE_DOM: 1.

Transferage: "Arthorn-broad ben-protoin kinase: AIP-binding: Coll Cycle:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. If here are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (Surchitle (Newworld)) in the site of Arabidous Profit in the statement of the stateme
                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00220;
                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00069; pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPK003527; MAP_kin.
InterPro; IPK002290; Ser_thr_pkinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:1346347; Mapk7.
InterPro; IFRU00719; Euk_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB019373; BAA82039.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1: FUNCTION: MEK5 AND ERK5 INTERACT SPECIFICALLY WITH ONE ANOTHER AND NOT WITH MEK1/EPF1 -P MEK2/EPF2 FATHWAYS (PY SIMILARITY) -1: ENZYME RESULATION. ACTIVATED BY TYROSINE AND THREONINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the nucleus.";
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"Achimation of the protein kinase ERKS/NMK1 by receptor tyrosine
Kinases: identification and characterization of a signification pribway to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
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Mammalia; Entberia; Rodentia: Sciurognathi; Muridae; Murinae; Mus
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DOMAIN: THE SECOND PROLINE-RICH REGION MAY INTERACT WITH ACTIN
TARGETING THE KINASE TO A SPECIFIC LOCATION IN THE CELL.
PTM: AUTOPHOSPHORYLATED ON THROUNINE AND TYROSINE RESIDUES, WHEN
THE C-TERMINAL PART OF THE KINASE, WHICH COULD HAVE A REGULATORY
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SIMILARITY OF PROTECT FINANCES
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••	HITTELLE LITTELLE LE	ALT CVERNAVY INSIRG ON PLAVA CLASAAZ HARRAŽBIJOTVILGI, AŽAAS HRBE.	THE GERLACHERUE GERFALLTANA LARTELE	SSI MACI KERAN HIST KIRAN METARAK KERANTAN METARAK METARAN METARAK	SSLÖADI BEFLIYLHSI.BIDYULUSILASAR SALW GUGGGARYAMGAALYI.IALIKANGEFVR		1 MRHIMARIFILGVIMALTEMOTTPEMISHIMEKIAQHIM PWMDRISLEHINPSIYVGLRI. 60	Scare 1779; OB 4; Length 400; Pred. No. 2.2e-146; P. Mismatches 14; Indels 21; Caps	SEQUENCE 400 AA; 44421 MW; 38059380F6110015D CRC64;	EMBL; BC011239; AAH11239.1;	Piladitoli (11 201) 1 to EMROJO dashi DBRI databases.		ANA: ASTIC GECOMERSHOGH MA WITH IN 196	SEQUENCE FROM N.A.	NCBi_faxID=9606;	Mammalia: Rutheria: Primates; Catarrhini; Heminidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens (Human).	UNKNOWN CPROPILIN FOR MICH 17407)	Of DEC 2001 (REMEDIE), 13, Last sequence update)	(Tremblrel, 19,		PRELIMINARY, PRT;	7.1.7 T

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Insights into the structural organization of the II inner arm dynein from a domain analysis of the I beta dynein heavy chain.";
Mol. Biol. Cell II:2297-2:13(2000).
EMH.; AL242523; CAB99316.1; ...
EMH.; AL242524; PANDODER:
                                                                                0 -DCT-2000 (TrEMBLIEL. 15, Last sequence update)
0 -DEC-2001 (TrEMBLIEL. 19, Last annotation updat
1 BETA DYNEIN HEAVY CHAIN.
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PROSTIE: PS00041: HTH_ARACLFAMITY_1: UNKNOWN_1.
PROSTIE: PS000215; MITOCH_CARKIER: UNKNOWN_1.
PROSTIE: PS000215; MITOCH_SAKIER: P2A4F10767FP5719 CP054;
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Bukaryota: Viridiplantae: Chlorophyta: Chlorophytoue: Volvocales,
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Perrone C.A., Myster S.H., Bower R
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InterPro: IPR000005; HTHArac.
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                                                                                                                                                                                                                                                 L.VVMSADI. - - - - - - - DLTFESLYAAKV
                                                                                                                                                                YFUSTSVI ACSTVEDVI KKAHFT STETYETQASLSGPYLTSVMGKAA--
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                                                                                                                                                                                                                                                                                                                         NAUMISQUUEVUNHKTYIDULIFFBCLAPRVMLEFAA·ETIFQTQEITSVTLQVUSLUFF 291
                                                                                                                                                                                                                                                                                                                                                                                                         FNLEEVMKAKADD-----PSALHVVI.---FQEVERVNALLVAVRRSCVELQRGIKG 4303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GYQQCLLGSAFSEDDGDCQGKPSMGQLALYLLALRANCEFVRGHKGDRLV-----SQL 131
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----GEREEWQLLEDPNTPLLQGIADYRPKIGETTF 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.7%; Score 110;
24.0%; Pred. No. 8
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                                                                                GELTAVLQTTARKASVPIDILSEE 4396
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Best Local Similarity 23.28;
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01-MAY-2000 (ITEMBLIEF: 13, Last sequence update)
01-DEC-2001 (TEMBLIEF: 15, Last annotation update)
PROBABLE CALCIUM-BINDING MITOCHONDRIAL CARRIER AT2G35800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ptam; PF00036; efhand; 1.
Pfam; PF00153; mito_carr; 3.
PRINTS: PR00926; MITOCARRIER.
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Bukaryota: Viridiplantae, Streptohyta: Embryophyta: Tracheophyta:
Spenmatophyta; Magnoliophyta, endicotyledons; core endicots; Rosidae;
eurosids II; Brassicales: Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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InterPro: IPP002067; Mit_carrier.
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InterPro: IPR002048; EF-hand.
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MEDLINE-20083487; PubMed=10617197;
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PROSITE; PS00215; MITOCH_CARRIER; 2.
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                                                                                               341 SLTELIE-----
76 TREGYDDOLLASARS PEROCHOLOGIO PORTO PORTO PORTO PEROCHAS PARTICIONES PEROCHES PEROCHES PEROCHAS PERO
                                                                                                                                                                                    16 ALTEMOS IPEMDSBLVEKLIGGBELLPWMOKLSLEHENESTYVIEKELSSEGAGTKEDLYEHS 75
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                                                                                                                                                                                                                                                                                   5.5%, Score 107; DB milarity 23.2%; Pred. No. 1.4; Conservative 47, Mismatches
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59 679
59 726
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                                                                                          ------LLPQLGRPSPDHPDKK-----KLISVQ-----DFFRYT-375
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l (POLENTIAL).
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SITE 1 (POTEN
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3 (POTENTIAL)
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        KX MEDLIN DERMELRY,

RA Adams M D., Colnikor S F. Holt P A., Evans C A., Gocayno J.D.,

RA Adams M D., Colnikor S F. Holt P A., Hoskins P A., Galle R.F.,

RA Adams M D., Colnikor S F., Hi P W., Hoskins P A., Galle R.F.,

RA Adams M D., Colnikor S F., Hi P W., Hoskins P A., Galle R.F.,

RA Adams M D., Colnikor S F., Hi P W., Hoskins P A., Galle R.F.,

RA George R.A., Lewis S E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G G., Royets Y.-H.C., Blazej P G., Champe M., Frifter B F.,

RA Barandon R.C., Royets Y.-H.C., Histor G.C., Mikios G.L.G.,

RA Barandon R.C., Royets Y.-H.C., Histor G.C., Mikios G.L.G.,

RA Abril J.F., Adbayani A., An H.-J., Andrews-Pfannkoch C., Haldwin D.,

RA Abril J.F., Adbayani A., An H.-J., Andrews-Pfannkoch C., Haldwin D.,

RA Ballew R M., Bassa A., Rozets G., Helt G., Nelson C.K., Mikios G.L.G.,

RA Abril J.F., Adbayani A., An H.-J., Andrews-Pfannkoch C., Haldwin D.,

RA Ballew R M., Bassa A., Rozets G., Helt G., Nelson C.K., Mikios G.L.G.,

RA Horkova D., Rotthan M B., Rozek J., Briskstein F., Brothic E.,

RA Horkova D., Rotthan M B., Rozek J., Briskstein F., Brothic S.M.,

RA Horkova D., Rotthan M B., Rozek J., Briskstein F., Brothack B.C., Chandra I.,

RA Horkova D., Rotthan M B., Rozek J., Briskstein F., Briskstein F.,

RA Durbin K.J., Evanschista G.C., Forraz C., Forriera S., Fleischmann W.,

RA Durbin K.J., Evanschista G.C., Forraz C., Forriera S., Fleischmann W.,

RA Glodek A., Gone F., Gorrell J.H., Gu Z., Godun P., Hurriss K.,

RA Horkin D., Houston K A., Howland I.J., Wol M., H., Herwander P., Horkov B.C.,

RA Lini X., Mattel H., Molnicsh T.C., Molney P., Hurriss I., Meskerti A.,

RA Mount S.M., Moy M., Marphy B., Marris I., Meskerti A.,

RA Mount S.M., Moy M., Marphy B., Marris I., Meskerti A.,

RA Mount S.M., Moy M., Marphy B., Marris I., Briskerti A.,

RA Mount S.M., Moy M., Marphy B., Marris I., Briskerti A.,

RA Mount S.M., Moy M., Marris G., Forra S., Pollard J., Drift W., Rosek K.,

RA Markinson D., Norra W., Mosary K., Norra W., Mosary K.,

RA Mount S.M., Moy
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01-MAY-2000 (TrEMBLiel. 13, Last sequence update)
01-MAY-2000 (TrEMBLiel 13, Fast ansorblies :pdat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pterygola: Neoptera: Endopterygola: Diptera: Brachycera: Muscomorpha:
Ephydroidea: Prosophilidae: Drosophila
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Eukary via Metal i Art' peda Tra
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Palazzolo M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DGAFQNALMISOLLFVLNHKTYID---1.1FPDCL
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Pittman
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C.S., Pan S., Pollard J., Puri V., Reese M.C
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RA Spier F., Shadr Flames I. Stepena M., Scheeler F., Shen H.,
RA Spier F., Spradling A.C., Stapleton M., Stepski M.P., Smith I.,
RA Spier E., Spradling A.C., Stapleton M., Stepski M.P., Smith I.,
RA Wang E. Y., Massarman D.A., Weinstock G.M., Mara A.H., Mara X.,
RA Williams S.M., Wendage F., Werley K.C., Wh.D., Yang S., Yao Q.A.,
RA Ye J., Yel E. F., Saveri H.D., Chan M., Chan G., Chan S., Chan G., Chan R., Chan C., Chan R., Myers E.W., Rubin G.M., Venter J.C.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RT "The genome sequence of Prosciphila melanogaster.";
RI Science 287:2185-2195(2000).
DR EMBL, AE003431 AAA45949-J.;
DR FlyBase; FBqn0029708; CG3556.
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MEDILINE 20196006; PubMed 10731132;

Adams M.P. Gelenker S.E. Holt F.A. Baskins R.A. Calle R.F. Andams M.P. Gelenker S.E. Holt F.A. Baskins R.A. Calle R.F. Andamatides P.G. Schurer R.E. Holt F.A. Baskins R.A. Calle R.F. George R.A. Lewis S.E. Birhards S. Ashbarner M. Hendersen S.N. George R.A. Lewis S.E. Birhards S. Ashbarner M. Hendersen S.N. Ritter C. B. Wernman F. Holt B. D. George M. Prolifer B.D. Ritterian C. Baskins G. B.C. Holt G. Nolson C.K. Miklos G.L.G. Wan K.H. Boyle C. Baxter B.G. Holt G. Nolson C.K. Miklos G.L.G. Mahl E.F. Ashbarner R. Baskins D. Balles B.M. Bask A. Baskinskill J. Hall Mahl Hardin D. Balles B.M. Bask A. Baskinskill J. Hall Mahl Hall Galt L. Boazley E.M. Becson K.Y. Bens P.V. Bernan B.F. Bhandari D. Balkaker S. Becson K.Y. Bens P.V. Bernan B.F. Bhandari D. Balkaker S.
                                                                                                                                                                                                                                                                                                                                                                                                        Pterygota; Neeptera; Endopterygota; Diptera; Brachysera; Mascomorpha;
Ephydroldea, Diosophilidae, Diosophila.
Nepi_TaxID 7027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota, Melanogaster (Fruit fly).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel, 13, Greated)
01-MAY-2000 (TrEMBLrel, 13, Last sequence of
01-JUN-2001 (TrEMBLrel, 17, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9VIH3;
                                                                                                                                                                                                                                                                                                                    STRAIN-BERKELEY.
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            419 LIGOVGLITABITHALGWEGEGAVEALQCOHVIBESSOFFENGEEKLAVPFGLESSAEESDA 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 KPT 11L16LAPYVI AUSSI CKOPKHEHSHIJI VATI CHBEPAQDI FEATITTI SANSSAAHVRI ROJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 TOPOGREGNYYSTULALŐEIMISEMROAELOTACIKARVALLASLÓDGARÓNALMISÓLIP 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            303 KRQTRRITIDIASGVINQSVBATAMVILALROTVTDH----RHRHIQHEVRRPARGLATIQ 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99 KF SMGQLALYLLALRANCEFVRGHKODELVS----
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RA Cherry J.M., Cawley S., Dablke C., Davepport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dablke C., Davepport L.B., Davies P.,

RA Dodson K., Doup L.E., Downes M., Dudan-Rocha S., Dunkov B.C., Dunn P.,

RA Dodson K., Doup L.E., Downes M., Dudan-Rocha S., Dunkov B.C., Dunn P.,

RA Dodson K., Doup L.E., Downes M., Dudan-Rocha S., Pleischmann W.,

RA Dotson K.J., Evangelista C.C., Ferraz C., Ferriera S., Pleischmann W.,

RA Hostin D., Houston A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA G.olek A., Gong F., Gorrell L.H., Gh. Z., Gelbart W.M., Glasser K.,

RA Hostin D., Houston K.A., Howland I.J., Wei M.-H., Ibeqwam C.,

RA Hostin D., Houston K.A., Howland I.J., Wei M.-H., Theqwam C.,

RA Kennel H.E., Kodina G.F., Kratt G., Kratt S., Krift D., Lai X.,

RA K., Lagvey J., Grift G.F., Kratt G., Kratt G., Morlis J., Moslicoli A.,

RA Neut S.M., May M., Murphy B., Murby J., Morny D.M., Moslicoli A.,

RA Neiter K., Wenindton K., Sannders R.D. C., Scheeler F., Shen H.,

RA Shion R.C., Sidon-Klamos I., Simpson M., Skupski M.P., Smith T.,

RA Shion R.C., Sidon-Klamos I., Simpson M., Skupski M.P., Smith T.,

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RA Shion R.C., Sidon-Riamos I., Simpson M., Skupski M.P., Smith T.,

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RA Shion R.C., Shipson R.C., Shipson R.C., Shipson R.C., Shipson R.C., Shipson R.C., Shipson R.C
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Best Local Similarity
Matchen 96; Conserv
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PROSITE: PS00037; MYB_1; UNKNOWN_1
SEQUENCE 846 AA: 93040 MW: B470
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                                                                                                   409 KKHLKLRESVIQTVATIT---
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364 -----KDGETTELRI, 373
                                                                                                                                                                                                                                                                                                    349 GAVQTFDAHNATFGFLYKESETTSEQLDLLEKYLQSLAVATHPDRKIVEHLFGLLEQESI 408
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                                                                                                                                                                                           KKAHPI GUFTYFTDASI SOPYI TSVMOKAAGEPEEWOLLEDPNTFLLDGIALIYEP----- 363
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DNA Res. 7:331-338(2000).
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Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
Mechicaki Y., Nahayama S., Yakacaki N., Shimpo S., Suqimoto M.,
Tabacaki C., Yamada M., Tabata S.:
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01-001-2001 (TEMBLE) 18, (ast sequence update)
01-001 2001 (TEMBLE) 18, Last annotation update
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Baeteria: Proteobaeteria: alpha subdirision: Rhizobiaceae group:
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InterPro; IPR001411; TCR_TetB.
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                                                                                339 GEREFWOLLROPULPILIOGI 358
                                                                                                                                                                 342 LIIVTGA-----LMIAAGIAĞEAYTIPLGSIPLILICALLQGGGGFGIAWFFUIRVIVASA 396
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                                                                                                                                                                                                                                                       296 ISVLAGSTVEDVLKKAHELGGETYETQ------ASLSG-----PYLISVMGKAA 338
                                                                                                                                                                                                                                                                                                                                                202 MIMVAALEVAIOSEGVYGPLILISLHEMPITTTSVITAAESTAWSILSTIVVANAPPORER 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     y Match 5.2%; Score 101; DB 16; Length 478; Local Similarity 24.1%; Prod. No. 2.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 ATVAGAAAGKIYSYVALKINMVVAALLYAAGALICATSESM-- QIFTAG-----KLIEG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EZ SZĘACI KEZLYTHSTWI GYĘTCI I GSAESPI GOROŻOKI SWOJI ALYTTALKAWCETYKO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 LARCHISLOILLHATMETMVALVMPAMVCELACVQLVCW·····-SLAIY··-ELG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 LGAFLEL-LGV-LGALTEMCETPEMÚSHLVEKLGQHLLPWMDRLSLEHLNESTYVGLRLS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VVLTAS - - - AGVDTALLRSSILTIVI.GLAGLALFFYTDALRPRSRLFPARLFSWRTPVGAG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYFTLGOAIMALAS -- FLVINIPS - AKKRETSAG----RIPPEPBAAL--ACLAVA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NISTPPOPITMAIPTVPEEITFACTFPGHPONVYSTPLALQFLMTSPMFGAELSTACLKAR 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               i., Sakabata 1., Sat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                        -----AETIP QTQEII --SVILQVLSLL: PPYRQS 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT:
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Hest Local similarity
Watches 56; Conserv
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KX MEDLINE-20016719; hubmod-Hill0712;

KX MEDLINE-20016719; hubmod-Hill0712;

KA Milte O., Alonso J., Altori H., Arabja P., Howang C., Brocks Y.E., Dewar K.,

KA Milte E., Clan A., Chav O., Chan B., Crossy T.B., Lewar K.,

PA Chung M. F., Cone L., Crossy A.B., Comary A.E., Crossy T.B., Lewar K.,

PA Chung M. F., Cone L., Crossy A.B., Comary A.E., Crossy T.B., Lewar K.,

PA Chung M. F., Cone L., Crossy A.B., Forg B., Fujil C.Y.,

PA Hunter II. Fankins J., Foldsyn-B., Flance M. F., Epster E.,

PA Hunter II. Fankins J., Coll., Lenc C.A., Lid., H., Lid., E.,

PA Langin-Hooper S., Lee A., Lee J.M., Lenc C.A., Lid., H., Lid., V.F.,

PA Lin M. Fin S., Him 7 A., Huros T.S., Mairi P., Marciali A.,

RA Militscher J., Miranda M., Nagyen M., Michann W.C., Osborne B.I.,

PA Militscher J., Miranda M., Nagyen M., Miranda M.C., Osborne B.I.,

RA Sahano H., Salvori S., Schwartz T.P., Shiom P., Sauthwick A.M.,

PA Militscher J., Vun Akon S., Vursborg G., Miranda M.J., Town C.D.,

RA Sahano H., Tallon L.J., Tambunga G., Turnui M.J., Town C.D.,

RA Sahano H., Salvori S., Schwartz T.P., Shiom P., Sauthwick A.M.,

PA Miltscher J., Vun Akon S., Vursborg M., Vrsoskala V.S., Walker M.,

RA Miltscher M., Vun Akon S., Vursborg M., Vrsoskala V.S., Walker M.,

Fraguence and analysis of chromosome I of the plant Arabidopsis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (IFEMHLTCL 17, Created)
01-JUN-2001 (TrEMHLTCL 17, Last sequence update)
01-001-2001 (TrEMHLTCL 18, Last annotation update)
HYPOTHETICAL 50.9 KDA PROTEIN.
FL8022.27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouso-ear cross).
Pukaryota: Viridiplantao: Steptophyla, Bmbryophyta, Tracko-phyla.
Spermatophyla: Marcellophyla: colorotylodon; corc.c.dlcots: Rosideurosids II: Brassicales: Brassicaceae: Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSTIF: PROGING PROTEIN_KINASE_ATH, CHKRENH_1.
PROSTIE: PS50011: PROTEIN_KINASE_DATH, THAT ASH, DATH ASKE, DA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0109; TYRKINASE.
SMART; SMC0210; STYC; 1.
SMART; SMC0210; TYFC; 1.
PAGETTY FOODOTT; FFOTFIELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro: IPR002240 Sor_thr_pkin
InterPro: IPR001245 Tyr_pkinase
Ptam PR00069 pkinase; []
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro: IPR000719; Euk_pkinase.
InterPro: IPR002340: Sor_*hr_p*inase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AC010926; AAG51840.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 408:816-820(2000)
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195 IPLA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              165 FYMERONLEGGI FQEYG-GALPWLIEVKILLIGAAKGIAFILHKQEKIYVIYMDEKESNI ---
                                                                 324 LEGKYSVEGIRKAAALAYOOL --- SHNPKSEPIMITVVETLEPILDLKDIQNGPF--VYI 378
                                                                                                                                                                                                                    264 SAGNLITMSDVESEGVVLLEMLTARKAVEKYHAQRGRNLVEWARFMLKDENKLERIIDES 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TKFDLYLHSLKLGYQQCLLGSAFS------EDDGD------CQCKP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COLUMBIA;
                                                                                                                                                                                                                                                                                          ------SMGQLALYLLALRANCEFVRGHKGDRLVSQLKWFLEDE---KRAIDTA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.2%;
dlarity 23.0%
Conservative 2
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                                                                                                                                       AMAGLAFTOLKRSNENPORRQRITMAIRTVREEILKAQTFEGHFGNVYS 154
                                                                                                                                                                                                                                                                                                                                                                   TI SECHESET S. H. D. ALD DELIGHELL CHILDVECTEGRAMICET | 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 100; DB 10: Length 450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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RESULT
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Bost bonal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 61, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0154; AMPBINDING.

PROSITE: PS50475; ACP DOMAIN; 3.

PROSITE: PS50455; AMP_RINDING; 3.

PROSITE: PS50415; PHOSPHOPANTETHEINE, CHKNOWN_3.

Chosphopantchheine.

SEQUENCE 4.447 AA; 452293 MW; 580A7F41522A0B05 CR054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterFro, IFR000873, AMP-bind.
InterFro; IFR001242; DUF4.
InterFro; IFR000379; Est_lip_thioest_actsite.
InterPro; IPP001601, Meth-transf.
InterFro, IFR000051; SAM_bind.
InterPro; IFR000051; SAM_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01 sell-2000 (TERMBLICH, 15, Created)
01 sell-2000 (TERMBLICH, 15, Last sequence update)
01-1957-2001 (TERMBLICH, 19, Last annotation update
ACTIGAMYCIN SYNTHETASE [II].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam: PF00501: AMP-binding: 3. Pfam: PF006648: Condensation: 3. Pfam: PF00975: Thioesterase: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Construction and in vitro analysis of a new blomodular polypeptide synthetase for synthesis of K mothylated anyl peptides."; Chem. Biol. 7.287\cdot297(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACMC.
Streptomyces chrysomallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF204401; AAI
HSSP; P14687; LAMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIRAIN ATCC 11523;
MEDILINE 2021/2879; FilhMcM-1078/9924;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q91.8H4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q91.8H4
                                                          2690 OWAPLPVQYADYTLWÖNELLGDQNDP 2715
                                                                                                                                      26 F2 AFBLABOFFLETELFEL
                                                                                                                                                                                                                 2579 LVSRHES------LRTVFPEVDGTPYQRLLTPEAAAPRLTVTPTSEADLPDALEAAARY 2631
                                                                                                                                                                                                                                                                                                                                                                      2476 GHSLLATRLTAQTRALFGVELELKSLFEGPTPAAVAARLDTAGPGRLALTVQERP----- 2530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interfro; IPR001031; Thioesterase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schauwecker F., Ptenniq F., Grammei N., Keller U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIRAIN ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID-1899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Actinomycetales: Streptomycinese; Streptomycetacese; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria, Firmicutes, Actinobacteria, Actinobacteridae,
                                                                                                339 -----GEREFWQ--LLRDPNTP 353
                                                                                                                                                                                                                                                   224 LASIQUOAFQNALMISQUIDVINHKTYIGLIFPUCLAFRYMLEFAAET-IIQIQEIIISVT DUD
                                                                                                                                                                                                                                                                                                                             164 REQETIMATE DATE TARGETTO HIGH SAVYSTERAL JEINT STRILGASELSTALIEARVAL 223
                                                                                                                                                                                                                                                                                                                                                                                                        TELL CHE CLEUVELIK WELELEKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   379 VPVA 382
                                                                                                                                                                         283 LQVLSLLPPYRQSISVLAGSTVEDV-LKKAHELGGFTYE---TQASLSGPYLISVMGKAA 338
                                                                                                                                                                                                                                                                                       ---ATMER STAGRETMENHEMISTER SATYNIET AT EL-----SODITARDALED 2578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   \Lambda\Lambda F42473.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                22.98;
                                                                                                                                      SAFEHVILLIVVIHLIACIOMSEGPLASINIARANAARAEGRAP 2689

    Mismatthes 109, Indels 59,

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Před. No. 6
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015074 1D 01

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PRELIMINARY;

PRT;

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Q90594
AC Q000
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                                                                                                                                                                                                                               01:JIN-2001 (FrEMBLICE), 17, Greated)
01:JIN-2001 (FrEMBLICE), 12, Last sequence update)
01:DEV-2001 (FrEMBLICE), 19, Last annotation update)
METAL-THANSFERFLING ATRASE LIKE ERCTEIN.
ATSG21930.
                                          Atabidopsis thaliana (Mouse-ear cress).
Eukuryotti Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: eudicotyledons; core eudicots: Rosidae:
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01-:AN:1998 (TrEMBLrel: 05, Last sequence update)
01-:DEC-2001 (TrEMBLrel: 19, Last annotation update)
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DNA Res. 4:141 150(1997).
eurosids II; Brassicales; Brassicaceae; Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       090534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1137 WKMKAQGATAMASI---AKQTSSLVPPYLGMILTALLQGLAGRTWAGKEELLKAIACVVT 1193
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Taneka A., Kotani H., Nomura N., Ohara O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE 97349984; PubMed 9205841;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          257 DCLAPRYMLEDAAETIPOTOEIISVTLOVLSLLPPYROSI--SVLAGSTVEDVLKKAHE 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    215 ACLKARVAL-LASLQDGAFQNA------LMISQLLPVLNHKTY------IDLIFP 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               845 RTTAALLPOLLDKGMMSTVTEVRALSINTLVKISKSAGAMLKPHAPKLIPALLESLSVLE 904
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Best Local Similarity
                                            SEQUENCE FROM N.A.

MEDILINE=21082081; FabMod-11214418;

Madsen O., Scally M., Locady C., Kao D., DeBry R., Adkins R.,

Amrine H., Stanhope M., de Jond W., Springer M.;

"Parallel adaptive radiations in two major clades of placental mammals."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (IrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation updat
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Frim: PR00702: Hydrolase: 1.
PRIME: PR00719: CATANPASE.
EBUSITE: PS00154. ATPASE_E1_E2.
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Rudd S., Lemcke K., Mayer K.F.X.;
Schmutted (MAF 2001) to the PMF, Benkerk, Didd databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bikaryota; Metazoa; Chordata; Graniata; Vertebruta; Enteleostomi;
Mammalia; Entheria; Perissodaetyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Equus caballus (Horse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9BDV4;
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InterPro; IPR001454; Hydrolase.
Nature 409:610-614(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID: 9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BRCA1 (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   408 NAAPVORLADATAGPEVYTIMSLSAMTEAFWYYVGSHTEPDVLLNDIAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   372 KL 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        317 FIVERDA SLSCHYLTSVMCKAMGEREFWOLLIDDHUD--LLQCLADYRPKINGELLEL 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  262 PVMLBBV---VELLBÖ-LÖĞLLANLIĞALISINĞEL AKARISISING KENAKKAHETÇEL 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299 SSDNNTPVDSVLSSDSTCTNVSVDD------TRVGDSLLVLFGET-----FPVDGSVLAG 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            215 --- AFGKRSPNMNSLVGLGSMAAFSIS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      168 SHILHSLGIHIAHGGIW-DILHNSYVKGGLAVGALL--- GEGRELLFEGIK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POVERAMMALISELESMECTES VALIS INTRA COMMINICADA A CARACARA A SA CARACAMANTE SA CAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGSALSEDEGEGEGGGKFSMGQLALYLLALPANCEFVPGHKCFFFTVSQLKWELEBEKKATEF 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPMPGAFIRTACIKAPVALIJASI OPRAFONALMISQLIJPVIJHKTYHIJIJIPP---HRIJAP 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.1%; Score 98.5; IB 10; Length 856;
21.0%; Pred. No. 8.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62; Mismatches 145; Indole
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UNKNOWN_1.
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       RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

RA White O., Alonso J., Altafi H., Arajo R., Bowman C.L., Prooks S.Y.,

RA Buehler E., Chan A., Chao Q., Chen H., Cheuk K.F., Chin C.W.,

RA Chung M.F., Chen I., Cheway A.R., Cheuk K.F., Chin C.W.,

RA Chung M.F., Chen I., Cheway A.R., Cheuk K.F., Chin C.W.,

RA Chung M.F., Chen I., Cheway A.R., Cheway A.F., Cheusy T.H., Chewat E.,

RA Chung M.F., Chen I., Cheway A.R., Fong R., Dujii C.Y.,

RA Hanter T.F., Chel A.D., Haas B., Hansen M.F., Hughes B., Hulzar L.,

RA Hanter T.F., Lee A., Lee J.M., Lenz C.A., Lij J.H., Li Y.-P.,

RA K. Kim C.J., E.-. H. T., Lee A., Lee J.M., Lenz C.A., Lij J.H., Li Y.-P.,

RA Lin X., Liu S.X., Liu P.A., Liuces J.S., Maiti R., Marziali A.,

RA Militscher T., Lee A., Lee J.M., Lenz C.A., Lij J.H., Li Y.-P.,

RA Militscher J. Lee A., Lee J.M., Lincran W., Cherce H.I.,

RA Sakano H., Salzery S.L., Schwartz J.R., Shinn P., Southwick A.M.,

RA Sun H., Tallon L.J., Tambunga G., Torium M.J., Town C.D.,

RA Wu D., Yu G., Fraser C.M., Vetter J.C., Davis R.M.,

RGequence and analysis of chromosome 1 of the plant Arabidopsis
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouso-ear cress).
Eukaryata, Viridiplantie, Streptophyta, Edbryophyta, inchcophyta:
Spermatophyta: Magnoliophyta: endicatyledans; eare endicats, Eusidie,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLEEL 17, Created)
01-JUN-2001 (TrEMBLEEL 17, Last sequence update)
01-JUN-2001 (TREMBLEEL 17, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       090714
090714;
                                                                  Nature 408-816-820(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-CV. COLUMBIA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOCHROME P450, PUTATIVE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    608 REGUNAL PERMANDARIAN PROBLEM PROPERTY PROPERTY NAMED 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 QTPEGHFG-----NVY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      528 PYLISVMGKAAGEREFW
                SIMILARITY: BELVINGS TO THE CYTOCHROME P450 FAMILY L: AC074025; AAS51161.1; .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIPQTQETTSVTLQVLStLPPYRQSTSVLAGSTVEDVLKKAHELGGFTYETQASLS---G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----ELLTANKHGISONPYY1PSLSPIRSSVKIVOOKNLPEGKILELOSLSP--E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              II; Brassicales; Brassicaceae; Arabidopsis.
    1871160JAdl
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Cyt_P450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94; Scoro 95; DB 6: Length 942
19: Pred: No. 19:
45; Mismatches 113; Indels
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Matches 67, Conserv
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                                                                                                                                     HSSP: 016539; [WFC. Mapk7. Mapk7. MCD; MCT:1346347; Mapk7. McP. pkinase. 15-berg; 19bergeriq: Pre_pkinase. InterPre; 1Pk903527; MAP_kin. InterPre; 1Pk903716; RNA_pol_omeda. InterPre; 1Pk903716; RNA_pol_omeda. InterPre; 1Pk903716; RNA_pol_omeda.
                 Pfam: PF00069: pkinase; 1.
PRINTS: PR01217; PKICHEXTERSN.
SMART; SM00220; S_TKC; II.
PEGGTTE: PS03351: MAPK: UNKNOWN_1.
PROSITE: PS50011; PROTEIN_KINASE_DOM: 1.
PROSITE: PS00108: PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                    MEDIINE 21179132) PubMed-11139578;
Yan C., Luo H., Lee J.D., Abe J., Herk H.C.;
"McHecvular Clerin, of Money ERKS_PMK1 2files Variants and Characterization of ERKS Functional Domains.";
J. Biol. Chem. 276-19879-19878(2001).
SEMILARITE BLOWES: Frint Sir/TBE FAMILY OF FEJTOTA EINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NoV-1999 (IrEMHSTel. 12, Created)
01-NoV-1999 (IrEMHSTel. 12, Last sequence update)
01-NSY-2001 (IrEMHSTel. 19, Last annotation update)
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PRINTS: PK00385; P450.
PROSITE: PS00086; CYTOCHROME_P450; UNKNOWN_1
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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ATP binding, Kindse, Serine/threenine protein kindse, Transferase
                                                                                                                                                                                                                                                                                     EMBL; ALLONDO; AADR9395.1; -.
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SEQSERGE 181 AA; 54311 MW; C838515B9A358F24 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142 IDTAAMAGLAETCUKESNENPGERQEITMAIRTVEEE-----ILKAQTPEGHEGN 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      266 -YYTDHTIKGTMLSLILAGTIYISAVTLEWALSSL------LUNPEYLKKVRDEIDNQIG 317
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747 AA;

80624 MW; AA270EA06F55F315 CRC64;

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WESTLET 14

USANAS

TO OSA-VAN

DE OSA-VAN

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Best Local Similarity
                                                                                                                                                                                                                                                                                                         Nieuman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Elsen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Procka I., Nelson W.C., Newton A., Sewhons C., Phadke N.D., Ely B., Deboy R.T., Lodson P. I., Durkin A.S., Gwhon M. I., Haft D. H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Ulterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., Whire O., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.; "Complete genome sequence of Caulobacter crescentus."; Proc. Natl. Acad. Sci. U.S.A., 98:4136-4141(2001)
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01-HN-2001 (TrEMBLrel, 17, Last sequence update)
01-BC-2001 (TrEMBLrel, 19, Last admotation update)
PENICILLIN-BINDING PROTEIN, la PAMILY.
                                                                                            Interpro; [PR001254; Transq1ycosy]
Ptam: PF00912: Transq1ycosy]: 1
Probom: PD001895; Transq1ycosy1; 1.
SEQUENCE
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          794 AA:
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     84395 MW; BE4147CA4E0675CD CRC64;
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Pred. No. 18,
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                                 PEAM; PE00069; pkinase; 1.

PPINTS; PR01217; PR1CHEXTENSN.

SMAPT; SM00220; S. TKC; 1.

PR0SITE: PS01351; MAPK; UNKNOWN_1.

PR0SITE: PS02157; FG0TEIN_KIHASE_AIF; 1.

PR0SITE: PS00169; PR0TEIN_KIHASE_ST; 1.

PR0SITE: PS00169; PR0TEIN_KIHASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammaila: Eutheria: Modentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                  Characterization of ERK5 Functional Domains.":
J. Biol. Chem. 276:10870-10879(2001).
! SIMILARITY: BELONGS To THE SER/THR FAMILY OF PROTEIN KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1999 (TrEMBLIEL 12, Created)
01-NOV-1999 (TrEMBLIEL 12, Last sequence update)
01-NEW-2001 (TrEMBLIEL 14 last annotation update)
ATP-binding, Kinase, Serine/threonine protein kinase; Transferase
SEQUENCE 806 AA; 87977 MW: 642593C7448D7001 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21179132; PubMed=11139578;
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                   InterPro: IPR002965; P_rich_extensn.
InterPro: IPR002290; Ser_thr_pkinase
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InterPro: IPR003527; MAP_kin.
                                                                                                                                                                                                                                             HSSP; P24941; 1HCL.
MGD; MGI:1346347; Mapk7
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Molecular Cloning of Mouse ERK5/BMK1 Splice Variants and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      514 PGSAFKLFYYLAALRECHTYTTPILLYTPYLYSCYMDKHFGKYHAPFYDI ITAFAGSSNV 573
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22.9%; Pred. No. 20
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Search completed: September -4, 2002, 11:48:26 Job time: $7624~{\rm sec}$

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Title:
Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Canola palmitoyl-A	AAR92788	1,7	328	4.5	86.5	39
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Soybean palmitoyl	AAR92785	, J	(3) (3)	(n	87.5	ند
Drosophila molamog	ABB69422	t s t s	5322	<u>ئ</u> رس	88	t)
Movel human prote	AAE09818	13	1127	4.6	88.5	31
Movel human	AAE09840	ta ta	11 E	, <u></u>	සහ . ි	Ö
Novel human	AAE09846	t 3	1092	<u>. 6</u>	. 39	50
Novel human	AAR09840	۲.	1097	4 6	2 86	ς. α
Novel human	AAE09844	(1 (1	1043	<u>-</u>	88.5	-1
Norel human	AAE09838	tu tu	1042	خبر (۲۱	e9.5	CT:
Novel buman	AAE09854	13	196	4.6	88.5	10
	AAE09852	(1 (1	926	4.6	88.5	دا
Novel human protei	AAE09850	t)	877	1.6	88.5	U.
Prosophila melanoq	ARR65242	ر: د:	3600	4.6	68	•3 •3
A Eumas ATR protei	AAW84271	50	1044	.~	9.0	-
Human ataxia and r	AAW13152	18	2644	4.7	9.0	20
Gell dydie Jhe-Epo	AAW19704	 D	2480	د	0.0	7
Cell cycle	AAW19723	ببر 00	2410	4.7	90	1.8
Drosophila melanoq	ABB60750	t)	5162	جب ل -	91.5	. 7
prosophila	APB70837	t)	1719		91.5	16
Rat NIS.	AAB73921	ca Cd	618	4.8	93.5	5
Rat sedium/iodide	AAW32105	(D)	618	<u>.</u> မ	13.51 51	44
	ABC01949	ci Ci	:п (-) (-)	•÷ ∵	94.5	
Human PRO4398 poly	AAU12232	(1 (1	(A)	(0	Т.	t-

VI ICHMENTS

E AARTRICE KLADINI ET TERREL 158 AA.
AAB58138;
14-MAR 2001 (first entry)
lung rations associated polypophido soquence SBJ to 476.
Hidean limit common associated protoing specimentoring outpotation
cardiogetive, immunemedicatory, magnifur active, valoerary,
pasts distinctly magnetaged, antilisted inc. gymeoclogical;
antibacterial; diagnosis; neural disorder; immune disorder; reproductive;
produteralize dissident; would heating; intentions disease.
Homo sapiens.
W0200055180-A2.
21 - SED - 2000
08-MAR-2000; 2000W0-US05918.
(BORA) BOMAH GUROND SCI INC. (ROSE) ROSEN C A.
Ruben SM;
WP1, 2000 587514,755.
N-PSDB; AAF18014.

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AAG00285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ouery Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunomodulatory; muscular active general; valuerary; gastrointestinal general; nephrotropic; antiinfective; gymecological; or antibacterial activity. The invention also includes antibodies specific for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polymnetestide sequences AAF17982 - AAF18424 serveds human lung cancer associated proteins represented in AAB58106 - AAB58548. Lung cancer associated proteins and polymnelectide sequences, their agonists, and antaqonists may have neuroprotective: cytosialie: cardicactive:
(GEST ) GENSET
                                                                                                          26-FEB-1999;
                                                                                                                                                                                                                                                                                                                               06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                         EP1033401-AZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06 CCT-2000 (tirst entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosome identification, as chromosome markers, and for numerous other disquostic or research purposes. The proteins may be used to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein or polynucleotide sequences. The lung cancer associated polynucleotide sequences may be used for detection of lung cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; Page 954-955; 1425pp; English.
                                                                                                                                                                                                               21-FEB-2000; 2000EP-0200610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene therapy; chromosome mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human secreted protein, SEQ ID NO: 4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAJC0285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA300285 standard; Protein; 54 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     identification and characterisation of the polynucleotide and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 219 yavepthqqhhsvdtaamaglaftelkrsnfnpgrr 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 GHKGDFLVSQLKWFLEDEKRAI-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 SSLQAGTKEDLYLHSLKLGYQQCLLGSAFSEDDGDCQGKPSMGQLALYLLALRANCEFVR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ~
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mrhlgatlillgvlgaltemceipemdshlveklgqhllpwmdrlslehlnpsiyvglrl 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5' EST, expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    268 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----DTAAMAGLAFTCLKRSNFNPGRR 165
                                                                                                          9908-0122487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41.6%; Score 803.5; DR 21; Length 268; 74.5%; Prod No 7 46-78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0: Mismatches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              were prepared from total human RNAs of polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3 untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5 ends of mRNAs and even in those cases where longer cCNA sequences have been obtained, the full 5 up is rarely included. 5 ESTs are derived from mPNAs with intact 5 ends and can therefore be used to obtain full length cDNAs and genomic towns one mapping procedures. They are used to obtain upstream chromosome mapping procedures. They are used to obtain upstream
Claim 1; Page 4-6; 10pp; Japanese
                                     quantitative analysis of
                                                        DNA sequence coding human intrinsic factor
                                                                                              P-PSDB; AAR32711.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid that is a 5^\circ expressed sequence tag (5° EST) for obtaining cDNAs and genomic DNAs that correspond to 5^\circESTs and for
                                                                                                                 WPI; 1993-070182/09
                                                                                                                                                                                                                             11-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                               Human; intrinsic factor; PCR; primer; polymerase chain reaction;
M13mp19; phage vector; stomach; cDNA library; probe; vitamin B12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JUN-1993 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR32711 standard, Frotein; 399 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAC00291
                                                                                                                                                     (KANF ) KANEKA CORP
                                                                                                                                                                                            11-JUL-1991;
                                                                                                                                                                                                                                                                     26-JAN-1993
                                                                                                                                                                                                                                                                                                          JP05015375-A
                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human intrinsic factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 13; SEQ ID 4366; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnostic, forensic, gene therapy and chromosome mapping procedures
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MRHLGAFLFILIGVLGALTEMCEIPEMDSHLVEKLGQHLLFWMDKLSLEHLNPSI 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.8%; Score 285; DR 21; Length 54
nilarity 100.0%; Pred. No. 5.2c-23;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                            91JP-0171062
                                                                                                                                                                                                                                 91JP-0171062
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                                         vitamin-B12
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                                                          used for
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This sequence represents bound intrinsic factor. The coding sequence was isolated by PCR using the primer sequences given in $\Delta\Delta Q37.410^{\circ}111^{\circ}$

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AAR32712
II) AAR3
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88882x3
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Best Local Similarity 25.2
Matches 10%; Conservative
          DNA sequence coding human intrinsic factor - used for quantitative analysis of vitamin-B12
                                                            P-PSDB; AAR32711.
                                                                                                                                           11-JUL-1991; 91JP-0171062
                                                                                                                                                                            11-JUL-1991;
                                                                                                                                                                                                                                                                        RAttus norvegicus
                                                                                                                                                                                                                                                                                                    Pat: intrinsic factor; PCE; primer; polymerase chain reaction; M19mp16: phogo vector; stemach, cDNA library, prob.; vitable E
                                                                                                                                                                                                                                                                                                                                                           Rat intrinsic factor.
                                                                                                                                                                                                                                                                                                                                                                                      17-JUN-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                            AAR 32712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR32712 standard: Protein: 421 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA sequence determined. This sequence was cloned from a human stomach clum library using the probes given in AAQ47312-13. Ham intrinsic factor protoin can be used for quantilize analysis of
                                                                             ₩ 28|\v2\v2\v2\v3\v4
                                                                                                          (KANF ) KANEKA COFP
                                                                                                                                                                                                            26-JAN-1993.
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                   JP05049478-A
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Chlamydia Pneumoniae
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                                                                                      DNA sequence coding human intrinsic factor - is used for cloning human intrinsic factor DNA using the new DNA as a probe
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RESULT ABB59988

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Best Local Similarity 22.7
Thomas 72. Conservative
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21-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 1239 1240; Disclosure; 1912pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome sequence of Chlamydia pneumoniae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pet_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ (D No 6756; 21pp + Sequence Listing; English.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insectionies, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ARL081676-ARL30511), expressed DNA sequences (ARL081675) and the encoded proteins (ARD081675737-ABB72372).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ 1D NO 1344; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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interactions :
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" AJ, Yang Y,
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                                                             Claim 10; SEQ ID No 226; 153pp; English.
                                                                                                                                      Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis, treatment of
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                                                                                                                     cancer, neurological, inflammatory disorders and for use in arrays for
                                                                                                                                                                                              N: PSDB; AAS44629.
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                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         furious types it directly to a magnetic value to be a sensitive set of a buman, documenter, mouse, hamster or rat. The disorders include cancers such as
AAU01777 standard; Protein; 750 AA
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                                                                                                                                                                                                                                                                                                                                                                                 257 DCLAPROMLEPAAETIPOTQETTSVTLQVLSLLPPVRQSI--SVLAGSTVETVLKKAHE 313
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20.0%; Pred. No. 1
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Human; secreted protein; immunoqeu; antibody; diagnosis; rheumatoid arthritis; hyperproliferative disorder; neoplasm; rheumatoid-arthritis; hyperproliferative disorder; neoplasm; cardiovascular disorder; cerebravascular disorder; neoplar ischaemia; angiogenesis; Alzheimer's disease; barterial interfen; viral interfication; fungal infection; corneal infection; wound healing; cell culture; epithelial cell proliferation; skin ageing; transplantation;
tissue regeneration; chemotaxis; food additive
                                                                                                                                                                                                Human secreted protein #56.
                                                                                                                                                                                                                                                                                                         AAU01777
                                                                                                                                                                                                                                                      18-JUL-2001 (first entry)
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Seq ences $\Delta AU27676$ - $\Delta AU28019$ represent tull-length polypeptides and contiq polypeptides of the invention. The proteins and their associated

DNA sequences are useful for the treatment, diagnosis and prevention of

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Best Local Similarity 20.2%; Fred. No. 0.75,
Matches 84; Conservative 65; Mismatches 144, Indels 126, Sups
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sumburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypoptides can also be used as a food additive or prosorvative to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Aluminut's discuse, intections caused by bacterial viruses and rungl and coular disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunosorbent assays (ELISA) Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              condition or susceptibility to a pathological condition. The antibodies can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polynucleotides, polypeptides and antibodics raised against them are used to provent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. The polynucleotides and antibodies are also used in diagnosing a pathological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nacicic acids encoding 37 human secreted polypeptides, useful for preventing, diagnosing and/or treating \phi q cancers. Farkinson's disease and diabetic retinopathy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPT: 2001-266150/27
N-PSDB; AAS02413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 471-473; 494pp; English.
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RESULT 11
ABG25767
                                                                                                                                                                                                                                     (II). (II) is useful for generating antibodies against it, detecting or grantitating a polypoptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving abertant protein expression or big-bytical activity. The polypoptide rad plynochrotic expression or applications in diagnostics, forensies, gene mapping, identification or mutations to grow the protein other types of data and product dependent on DNA and maintenance of the produce of the invention.

105(2021) ANNION TOTAL TOTAL ANNION TOTAL TOTAL ANNION TOTAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnostics, forensits, decembered, other traits and to assess responsible for genetic disorders or other traits and to assess
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specification, but was obtained in electronic format directly from WIPO x^* Or with (x,y) in (x,y) in the Letters constant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polyblehootides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (1) is useful in gene therapy techniques to restore cormal activity of (1) or no tent disease states irrelating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; SEC ID No 56126; 103pp; English
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diagnostics, forensies, gene mapping, identification of mutations
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Best Local Similarity

4.98; 20.78;

Score 94; DB 22; Pred. Mo. 4.7;

Length 1758;

Query Match

Sequence

1758 AA;

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09-DEC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human secretory and transmembrane, PPC: mammalian, cancer; land, breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; five fatty acid, skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human PRO4348 polypoptide sequence
18-FEB-2000;
18-FEB-2000;
                                                             06-JAN-2000;
11-FEB-2000;
                                                                                                                                                                                        20-DEC
                                                                                                                                                                                                                  16-1-EC-1999;
20-1-EC-1999;
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24-FEB-2000;
24 FEB 2000;
01-MAR-2000;
                                  of Tlymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCS), or the proliferation of endothelial cells. Some of the IRO feligeptides may modulate glucose or free latty and up the by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIA. The FRO polyceptides can be used in assays to identify molecules involved in binding interactions. The polynucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy.
                                                                                                                                                                                                                                                        polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tunour necrosis factor-alpha (TNF-alpha) from human blood, the
                                                                                                                                                                                                gene expression in perioyte coils, the release of proteodlycans from cartilage, the proliferation of inner ear utricular supporting cells or
                                                                                                                                                                                                                                                                                                                      PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO
                                                                                                                                                                                                                                                                                                                                                                               AAU12172 AAU12446 represent sovel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bioactive molecules to cells expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          other PRO polypeptides, link bioactive molecules to cells expressing 
[Re polypeptides, and detect the presence of mammatian through e.g.
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21-MAR-2000;
Sequence
                                                                                                                                                                                                                                         proliferation or differentiation of chandrocytes, the proliferation or
                                                                                                                                                                                                                                                                                                                                                              PRO polypeptides, to modulate biological activities of cells expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 12; Fig 122; 813pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lung, breast, prostate, cervical
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  511 AA;
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ME, Goddard A,
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, 2000WO-US14042.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.8%; Score 93.5; DB 22; Length 511; 18.5%; Pred. No. 0.77; ative 51; Mismatches 125; Indels 163;
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            polynuclectic describes are also used in diagnostic and expective target of the identifying agreement agreement in which displacement things of the restore normal artivity of (11) or the true displant in, detecting of (11). (11) is useful for generating antibodies against it, detecting of (11). (11) is useful for generating antibodies against it, detecting of quantitating a polypephide in tissue, as molecular weight markers and as a food supplement. (11) and its binding partners are useful in medical industry of sites expressing (11). (1) and (11) are useful for treating of indusing of sites expressing (11). (1) and (11) are useful in medical of disorders involving theorem prinches expressing a tribulation of the property of a reading the control of the prince intendity. On the property of a reading the control of mutations of diagnostics, forensics, gene mapping, identification of mutations of responsible for genetic disorders or other traits to assess biodiversity and the produce other types of data and produces dependent on DNA and on a mino acid sequences. Abbooth Abstrator represent cover bulbands of diagnostic amino acid sequences of the invention.

CC Mater The sequence data for this parant did not appear in the printed of specification but was obtained in electronic format directly from MIPC at tip-information of the printed produces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to isolated polynucleotide (1) and polypeptide (11) sequences. (1) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in
diagnostics, forensies, gene mapping, identification of mutations
responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and gene mapping, and in recombinant production of (II). The polynomial of idea are also used in diagnostics as expressed sequence tark
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23-AUG-2000; 2000US-0640167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the encoding cDNA sequence and antibodies that are immunoreactive with the sodium/lodde symporter can be used for the diagnosis of thyroid discretes such as hypothy; ddism, hypothy; odism, by the thyroid career in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated thy: id sodium, field be dymperter asked to develop products for the diagnosis and treatment of thyroid disorders, e.g.
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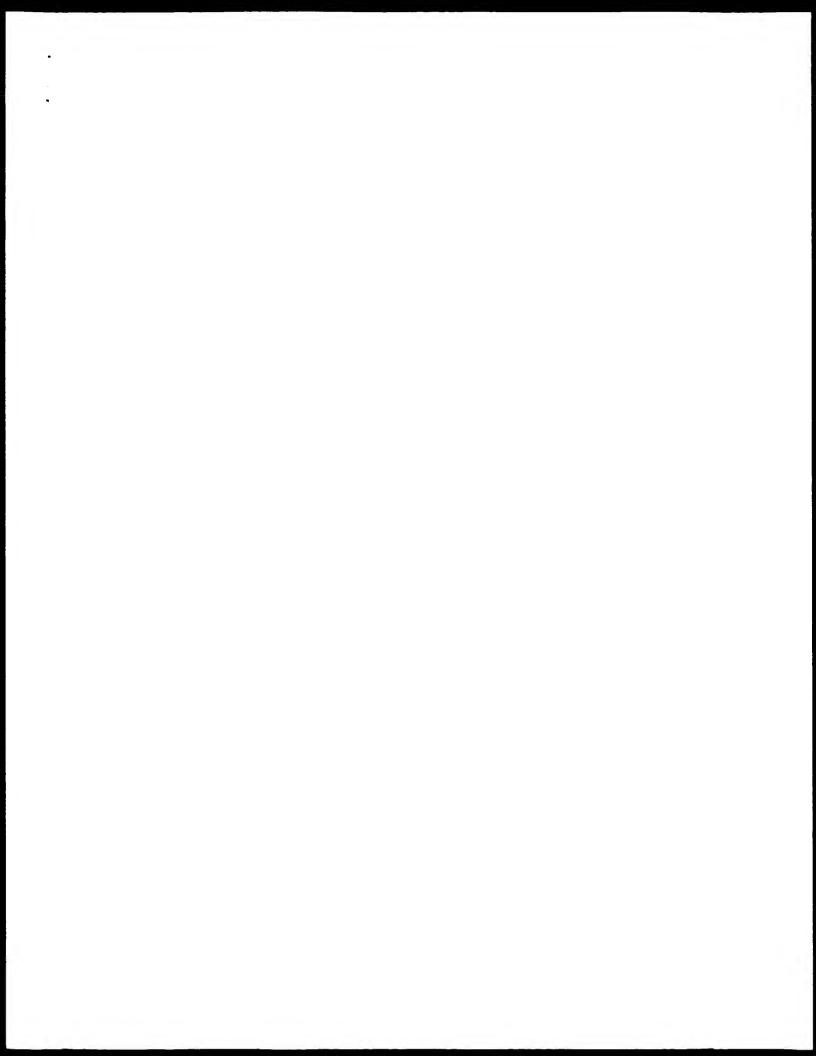
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    therapeutic gaps released fire belief into enthanciania many content into determining the location of labelled molecules which are transported into the matter beautifule. The matter periods a service than of the matter periods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Monitoring transgene expression and therapeutic paptide production in mammals by detecting marker polypaptides linked to transgenes of therapeutic genes released from cells into extracellular body fluid -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         quantifying or detecting the amount of marker polypeptide and/or sodium iodide symporter (NIS) linked to the product of the transgene or therapouting gene released fig. 1918 into estimate into Lody Huid, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is a self-clearing linker. It may be used in a method for monitoring expression and/or localisation of a transquee, and
                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                     into a cell, which does not adversely affect normal cellular function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   production of therapeutic peptide in a mammal. The method involves
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200 IMESEMBÇARI - CEACLKARVALLASI ÇERAFQNALKISÇIL - EVLKHKTYITILLEFE 257
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283138 seqs, 96089334 residues

Post-processing. Minimum Match 0% Maximum Match 1909 Listing first 45 summaries

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4: pir3: * PIR_71:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the retal score distribution.

SUMMARIES

87.5 4.5 1206 2 B87247	64 t 1 t 1 1 2 3 850841	87.5 4.5 396 2 B83461	87.5 4.5 363 2 AH2796	87.5 4.5 363 2 H97575	98.5 4.6 1459 2 A:2488	89 4.6 1810 1 TL1198	4 6 960 2 AFILER	89 5 4 6 1294 2 135044	89 E 4 F 302 2 A82080	90 4.7 1693 2 876086	91 4.7 836 2 AF3233	9] 4 7 DE DISERSON	4.8 1175 2 T45124	93 4.8 844 2 Ariagi	93.5 4.8 794 2 C87437	93.5 4.8 618 2 268513	93.5 4.8 481 2 B96691	97 5.0 2672 2 A48126	G96749	103 5 5 4 307 2 program	103 5 5 4 307 2 P86894	5.5 844 2 B84773	.5 9.5 416 2 \$09334	63.5 13.6 421 1 A34003	5 13 A 417 1 A39904	.5 13.9 417 1 A49684 q	.5 16.3 433 1 A34227 t	.5 97 5 427 1 A29744 t	NO. Store water for the F. H. H.
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Query Match. 97 78, Source 1983, 5, TP 1, Territh 427; Best Local Similarity 87.6%; Prod. No. 2.4e-156; Matches 374, Computation 0, Mismatches 2, Indels 51.

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ALIGNMENTS

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Pispecies: Homo sapiens (man)

Pillate, 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 08-Dec-2000

Cincression: A34227; A42174; A60553

R.Johnston, J.; Hollekens, J.; Allen, R.H.; Berliner, N.
J. Biol. Chem. 264, 15754-15757, 1999
A:Hitle: Structure of the cDNA encoding transcobalamin 1, a neutrophil granule protein. A:Reference number: A34227; MGID:89380156
A:Accession: A34227
                                                                                                                                                                                                                                                                                                                                           C:Superfamily: gastric intrinsic factor
E:1-24/Temain: signal sequence #status predicted <SIG>
E:24/443/Product: transcobalamin #status experimental <MATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Molecule type: protein
A:Residues: 24-25,'X',27-32,'X',34-38,'X',40 <TON>
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Seand, J. Clin, Lab. Hovest, 50, 187-194, 1990
A:Hille Epidermal growth factor and haptocorrin in masal secretion
A:Reference number: A60553; MUID:90251988
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A:Resicues: 1-26 -Jo2>
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A:Access on: A42174
A:Status preliminary
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R:Johnston, J.; Yanq-Fenq, T.: Berliner, N.
Genomics 12, 459-464, 1992
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A; Residues: 1-433 (JOH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A: Note: sequence extracted from NCB: backbone (NCBIN:95735, NCBIP:95736)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transcobalamin | precursor [validated] - human
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                                                                                                                                                                       Best Local Similarity
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                                        4 LGAFLFILGVLGALITEMCETPEMDSHLVEKLGQHLLPWMDRLSLEHLN-----PSTYVGL 58
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                                                                                                                          114; Conservative 69; Mismatches 153; Indels 117; Gaps
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25.2%; Fred. No. 2c
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DB 1; Length 433;
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A; Residues: 1-417 < LOR>
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Best Local Similarity
2)4 IKADG LIGD LYSTGLANQALSVTPHQPTKKWD-CEKTMHTILNETKQGKFQNPMSTAQTI. 272
                                                                                      183 QTEEGHEGNAKSTELALOFEMTSEMGOAELGTAT KARVALEASE OFGAROMISMISSOLL 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                     112 LEANCEPVECHKGDELVSQLK-W------
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                                                                                                                                                                            RESERVALKATVEKISER 213
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133 WELEDEKR------ALIVTAAMAGI AFTGI KRSNEN-----PGKRQKITMATKTVKEET 179
34] -RINETYPTNYTYLNGSYPLSYMEKAGKNYDTIFGFIMEESS WGAYIICIQGIGANNN 497
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                                                                                                286 LSLLPPYRQSISVLAGSTVEDVLKKAHELG----GFTYETQASI.SGPYLTSVM6KAA--G-449
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                                                                                                                                                                                           QVLFALMOKTI LDI NKORBOVSASONI NI SAD-+++++ EPTI VITPUSQSVI SVNYSV - 440
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J. Biol. Chem. 268, 26559-26570, 1993 A.Title. Use of transpers also U. Study regulation of speciety recoion in the parieta A)Reference number: A49684; MUID:94075347 A:Accession: A49684 qastric intrinsic factor precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C; Superfamily: gastric intrinsic factor C; Kepwords: glycoprotein; vitamin 812 transport; vitamin carrier A,Cross_references. CB.L24191, NID.4445091, FIBM.AAA47882.1; FID:4445992 Length 417,

17;

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A.Map position: Ilq12-llq13
C.Supertamily: gastric intrinsic lactor
C.Supertamily: gastric intrinsic lactor
C.Forwards alymorphis witerin R12 transport. Illatin existor
E.1-18/Memain: signal sequence #status predicted asign
E.1-18/Memain: signal sequence #status predicted asign
E.19-417/Memain: gastric intrinsic forth #status predicted
E.311, 430, 434, 437/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C:Species: Homo sapiens (man)
C:Date: 10.8cp-1999 #Sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A39904 A60437; $44128
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A:Description: A cDMA sequence of the haman intrinsic lactor
A:Reference number: 944129
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A:Regidues: 1-00 (2010) 117 (HA2)
A:Gross-references (MP) M10562, NDD (475642, FID) CMA51061 1, DID (470563
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A:Real Hors (1991/60/18/1971/1941/197)
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A;Accession: A60437
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Neyo, P : syendson, L: Bubber, D.; Olesen, H. Scand, J. Clin, Lab. Invest, 49(Suppl.194), 19-22, 1989
A)Title: Human intrinsic factor. Its primary structure compared to the primary structure
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A; Residues: 1-417 <HEW>
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A:Title: Human gastric intrinsic factor: characterization of cDNA and genomic clones
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                                     : Gordon, M.M.; Taggart, R.T.; Mohandas, T.K.; Alpers, D.H.
09 TPTCAATS BYTHETSTHUMMETTHECETABA HESUMARABLEAM
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R.Diockgraete, B.K., Seetharam, B., Dahamadak, L., Leykam, J.F.: Alpers, D.H. proc. Natl. Acad. Sci. U.S.A. 85, 46-50, 1988
Armitle: Isolation and structural characterization of a cDNA clone encoding rat qastr Armeterine number: A34003, MOID:88124816
A.Accession: A34003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qastric intrinsic factor precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Pate. 10 Sep 1999 #sequence_revision 10 Sep 1999 #text_change 10-Sep-1999
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                                2.5 Sperfamily, questric intrinsic factor
C.Keywords: qlycoprotein: vitamin B12 transport: vitamin carrier
Fil-22/Domain: signal sequence #status predicted (810)
                                                                                                                                                        A; Note: part of this sequence was confirmed by protein sequencing Community flux protein brude the relations studied to tabilitate receptor mediated
                                                                                                                                                                                                                                      A;Residues: 1-421 <DIE>
A;Cross-references: GB:U02577; NID:q204683; FIDN:AAA41261.1; FID:q204684
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P.23-121/Product. gastric intrinsic factor #status predicted RMAI
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Ξ. Ē <u>...</u> Ş <u>...</u> 5 2 ζξ. S Query Match 338 FARAKSUSVITAVI FEAURENHMERFETIMISWULLVESINALADAVAHALIMERI, SON 396 TALE OF THE AND AND THE SECOND STATES OF THE STATES OF THE SECOND 278 CHARLYTON GAT OF BHINTET DITOFFT AS LEXITAGED HANGLEGADITHMAN 1897 244 VENERTYTEL --- TERECLAPRYMER -- PAARTIPQTQETTSVITGV -- LSILLFPYRG 294 16) ALLMMOSSTESVOJOAVAJJACIOMYANJOVISJOMY - KOJEGJALAVIVUNIJERI 218 10.1 TIT PANCESTROHKODRIVSQIK-W------y Match 13.6%; Score 263.5; DB-1; Local Similarit, 24.0%; Fred. Mo. 5.5e-15; how 199, Gesservative 70, Wismatches 190; 11 YLLNVLWAVAGTSTRAQRSCSVPPDQQ------PWVNGLQLLMENSVTESDLFNP 59 9 FLIGVLGALT---TISSON DEGSAVS LUGANMUSWIESNEGAESSSEYGEALAILALOQKNSEATLEIAVEFA 163 STUMMILE SOMEON PRESIDENT CONTRIBUTION OF CITTISABETHORS SOME ENGINEERING AND THE PRESENT FOR A STATE OF THE ----- HMCETPEMDSHLVEKIGQHLLPWMDRLSL------EHLNP 52 · TYMEDA_BELLEY_LMASEZACE · MESHEWEGEE, FILMM (FIVELES) FAQ 183 DB 1; Length 421; indels 111. Caps TNOCLALLIMAL 103 17:

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A:Molecu e type: mRNA
A:Resiones: 1-416 - HEW -
A:Cross-references: FMRL :X52566; NID-q1963; PHENECAA 68800.1; PID:q1954
C:Superfamily: qustric intrinsic factor
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N.Alternate names: haptocorrin
()Species: Sus serota demosited (demosite pig)
()Date: (2-Feb-1994 #sequence_revision 12-Feb-1993 #text_cbange 20 Aug 1999
                                       R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Molidt, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
                                                                                                                                                            probable mitochondrial carrier protein (imported) - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: (2:Feb: 2001 #sequence_revision 02:Feb:2001 #text_change 02:Feb:2001
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AfAccess.on: S09334
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k:Hewitt J.E.; Seetharam, B.; Leykam, J.; Alpers, D.H.
Eur. J. Biochem. 189, 125-130, 1990
Nature 402, 761-768, 1999
                                                                                                                                      C: Accession: B84773
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Fishiral, M.; Hirakawa, H.; Kimoto, M.; Takuchi, M.; *ishi, F.; Ouchi, K.; Shiba, T.; nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of chlamydia pheumoniae J148.
A;Reference number: A86491; MUID:20330349
A;Accession: F86594
                                                                                                                                                                                                                                                                                                                                                                                                                                                       lipoate synthetase [imported] – Chlamydophila pneumoniae (strain J148)
CrSpecies: Chlamydophila pneumoniae, Chlamydia pneumoniae
CrDate: 32:Ma: 230] #sequence_rectsion 62:Ma: 2801 #3 xt_change 28 Mar 2001
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ArAccession: B84773
C; Superfamily: lipoic acid synthase
                                                                 C; Genetics:
                                                                                             A;Cross-references: GR:RA000000R; NID:g8979206; PIDN:RAA99040.1; GSEDB:GN00142
A;Experimental source: strain J138
                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-307 <STO>
                                                                                                                                                                                                                             A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                           C:Accession: F86594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-844 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              723 GLYAESKKMVAQALGRELEAWETI 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           663 LLGTAVRIPCEVLKQRLQAGMENNVGEAIVGTWKQIWJPSGFERGTGATLCREVPLYVVGM 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              602 GLRTGIFEASKLYLINEAPNLPFIQVIIII.YSLFGWFRQDSNFVLQVQSI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 KW----FLEDEKRAIDTAAMACIAFT---CIKPSNE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             327 GPYLTS - - VMGKAAG - EREFWQLL 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                299 LAGSTVE---DVLKKAHELG-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              547 AGGLASALSTSLMHPIDTIKTRVQASTLSFPEVIAKLPEIGVRGVYRGSIPAILGQFSSH 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             229 DCAFQNALMISQLLPVLNHKTYID---LIFPDCL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 I KAQTPF----GHEGNVYSTPI ALQELMTSPMB-GAELGTACLKA-RVAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       341 SLIELLE ---- DEFRYT 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TE EKECYÇÇCILGSAFSENIGIYÇEKISMEÇLALYE---LALFANCEFYPÇIIKGIYI VSÇE İST
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Query Match Best Local Similarity

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Score 103.5; DB 2; Pred. Mc. 0.30;

Length 307;

	OY 180 LKAQTPEGHEGNYYSTELALQELMISPMPGAELGTACLKAPYALLASIQNQAEQNA 235
	OY 125 PRIVEY EMPLEMENTATION AND CLEAR AND CLERK HIMPORNOW TIME TENDED 179 170
	UY 86 GSAFSEED
18;	Ouery Match 5.4%; Score 103.5; DB 2; Length 307; Best Local Similarity 22.4%, Prod N. 0.30; Matches 72; Conservative 47; Mismatches 87; Indels 115; Gaps
1. mu.g18999	A.Molecule type: DNA A.Residues: 1-307 <rea. (7189956,="" 1-307="" <rea.="" a.experimental="" a.gene:="" a.gress-references:="" a.residues:="" ar39,="" c.genetics:="" cells="" eigh.am:3981).="" gp1038="" gp1038<="" gr-apogree,="" hip:="" hl="" lipa;="" source:="" strain="" td=""></rea.>
All Pib.q437714 a b. Hickey, G./ Calchery, Jun-Tip / Kast	A;Moleculo Type: DNA A;Rosidues: L-407

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A:Accession: G96749
A:Status: preliminary
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A.Authors. Salzberg, S. L. Schwart, J.P.; Shinn, P.; Soathwick, A.M., Sun, H.; Tallu ker, M., Wu, D., Yu, B.; Fraser, C.M., Veller, J.C.; Sacks, E.W.
A.Tille: September and apalysis of chromosome 1 of the plant Arabidopsis.
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A:Map position: 1
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Nature 408, 816-820, 2000
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CrSpecies: Arabidopsis thaliana (mouse-ear cress)
CrDato: 02-Mar-2001 #sequence_revision 02 Mar-2001 #text_chapte 31 Mar-2001
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A.Gross-references: GP:AEG05173; NID:g6648174; PIDM:AAF21174.1; GSPDB:GN00141
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379 VPVA 382
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translation activator GCNI - yeast (Saccharomyces corcuisiae)
NAItormate names: protein G1918; protein YGL195w
C:Species: Succharomyces occovision
C:Date: 21:Jan:1994 #sequence_recision 18 Nov 1991 #text_shand: 21 Jul 2000

RESULT 11 A48126

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A:Molecule type: DNA
A:Molecule type: DNA
A:Residies: 1:272 kKL2
A:Bross references EMN: X91837, NIB::gl177627, FIE:E293621, FIE::gl177633
A:Experimental source: strain FY1679
R:Bruschi, C.V.; Coglievina, M.; Hertani, I.; Klima, R.; Zaccaria, P.; Delneri, D.;
R:Bruschi, C.V.; Coglievina, M.; Hertani, I.; Klima, R.; Zaccaria, P.; Delneri, D.;
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A:Moslidues. I 2672 -MAR*
A:Rossidues. I 2672 -MAR*
A:Ross-references: EMBL:L12467; MID:gR12009; FICM:AAAR4435, L: PID:g311109
A:Rose-references: EMBL:L12467; MID:g811009; FICM:AAAR4435, L: PID:g311109
A:Rose-references: EMBL:L12467; MID:g811009; FICM:AAAR4435, L: PID:g811109
A:Rose-references: EMBL:L12467; MID:g811009; FICM:AAAR4435, L: PID:g811109
A:Rose-references: EMBL:L12467; FICM:AAAR445, L: PID:g811109
A:Rose-references: EMBL:L12467; FICM:AAAR445, L: PID:g811009
A:Rose-references: EMBL:L12467; FICM:AAAR445, L: PID:g811009
A:Rose-references: EMBL:L12467; FICM:AAAR445, L: PID:g811009
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A:Reference number: S62045
A:Accession: S62050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RyMarton, M.1; frouch, P.; Hincobusch, A.C.
Mol. C-Ul. Biol. 13, 3541-3556, 1993
A:Fittos GrNI, a translational activator of GCN4 in Saccharomyces corovisiae, is require
A:Reference number: A48126; MUID:93268304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E:1704-1720/Demain: transmembrane #status prodicted cTMS>
E:2021 2007/Demain: transmembrane #status prodicted cTMS>
E:2272 2008/Demain: transmembrane #status prodicted cTM7>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F:69-85,5 multiple transmembrane #status predicted < IM1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A: Map position: 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A: Experimental source: strain $2880
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                                                                                                                                  1948 FQ--
                                                                                                                                                                                                                                                                                                                                                      1891 AQTLGDLVRRVGGNAL--SQLLPSL-EESLIETSNSDSRQGVCTALYELIESASTETISQ 1947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         335 GKAAGEREEWQLLR- ----DPNTPLLQGIADYRPKDGETI 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            221 VALLASIQDGAFQNALMISQLLPVLNHKTYIDLIFPD-----CLAPRVMLEPAA-ETIPQ 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 LLGVIGALTEMOETPEMD------SHLVEKLGUHLLPWMDELSLEHLNISTYV 55
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                                                                                                                                                                                                                                            TQEIISVTLQVLSLLPPYRQSISVLAGSTVEDVLKKAHELGGFTYETQASLSGPYLTSVM 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MATRITUREE - - - ILKAOTPECHFONVYSTPLALOFLMTSPMPO - - - - - AELGTACLKAR | 220
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                                                                                                                      --STIVNIIRTALIDESATVREAAALSEDVEQDVV 1982
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A;Authors: Hunter, J.L., Jenkins, J.; Johnson Hepson, C.; Khan, S.; Khaykin, E.; Kim, C.A., Li, J.H.; Li, Y., Liu, X.; Liu, Z.A., Lurvs, J.S., Maiti, R.; Marzia Kille, M.; Escurey, L.; Esweley, L.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.P.; Shinn, P.; Senthwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; bavis, R.W. A;Ittle: Sequence and analysis of chromosome i of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Map position: 1
C.Superfamily, human cytochrome P450 CYP2D5; cytochrome P450 homelesy
C:Keywords: heme; iron; metalloprotein
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E;Theologis, A.; Ec
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C:Species: Arabidopsis thaliana (mouse-ear cress)
C.bate: 02 Mar 2001 #sequence_recision 02 Mar 2001 #text_change 20-Apr-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F,416;Binding site, heme iron (Č73) (axiai ligand) ≢status predicted
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Best Local Similarity
Matches 67, Conser-
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                                                                                                                                              1.12 TETAAMAGLAETCLKRENFNFGEBORTTMATETVEEE
                                                                                                                                                                                                                                                                                                            174 KCYYGDG AFDDEE
       DD4 KKIAAKLUEEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.89; Score 93.5; LB 2; Longth 481;
nilarit; 21.88; Fred. No. 4.6;
Conservative 45, Mismatches 103, Indels 93, Caps
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thyroid iodide transport protein - rat
C:Species: Pattus norvegicus (Norway rat)
C:Date: 29 Jan 1998 #sequence_revision 06
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A; Reference number: $68513; MUID: 96158880
                           A: Title: Cloning and characterization of the thyroid iodide transporter
                                                       R;Dai, G.; Levy, O.; Carrasco, N. Nature 379, 458-460, 1996
                                                                                                                    C; Accession: S68513
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                                                                                                                                                                                                                                                                     RESULT 13
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                                                                                                                                             06 Feb 1998 #text_change 05 Nov 1999
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251 TDLTEPROCLAPPOMERPAAETTPOTOFFTSVTLOVE ---STEPPYPOSTSVLAGSTVEDV 307

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R:Nierman, N.C.: Feldblyum, T.V., Paulsen, I.T.: Nelson, K.E.: Eisen, J.: Heidelberg, J. B.: Laub, M.T.: DeBoy, R.T.: Podson, R.P.: Putkin, A.S.; Gwien, M.I.: Haft, D.H.: Kolod n, J.: Ermolaeva, M.: White, O.; Salzberg, S.L.: Shapiro, L., Vente:, J.C.; Fraser, C.M. Proc. Natl Acad. Sci. U.S.A. 98, 4176-4141, 2001.
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Peference number: A87249: MIID:21]73698: PMID:11259647
A:Accession: C87437
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F:194-729/90sion: brucino hippor
F:242 261/20smain: transmembrane #status predicted <7M7>
F:287 307/20smain: transmembrane #status predicted <7M9-
F:341-367/20smain: transmembrane #status predicted <7M9-
F:4417-437/20smain: transmembrane #status predicted <7M9-
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E:205 [495]497/Pinding site, early hydrate (Asc.) (covalent) #status prodicted
E:551/Binding site, plosphate (Ser) (covalent) (by cAXE dependent kinase) #status prodic
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A:Cross-references: hyperid decimed only the FMT 5
C:Keywords: glyceprotein lennine ripper; plospherochein; thyroid hormone blosynthesis; F:12 3f (Complet Cine Estates Fire) decimed blosynthesis;
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A;Molecule type: mRNA
A;Residues: 1:618 <DAT>
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A; Residues: 1 704 //STO
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289 QOLAKNAFISSDENI.FEKAQEALTAVYLEARTSKDETTSPYLSSVYFGDGAEGLPAAARH 349
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A;Molecule type: DNA
A;Molecules: 1 844 <KUR>
A;Poss references: GB:PA000019; PIDN:BAB73355.1; PID:g17120745; GSPDB:GN00179
A;Cross references: Strain PCC 7120
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A.Titlo Complete Samonio Sequence of the Filamentous Kitrogen Lixing Gyanobacterium A.Feference nomber, AR1807, MUTD 21525285, PMID-11750840
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CrSpecies: Anabaena sp.
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ALIGNMENTS

COMMENT RESULT BC001176 REPERBER SCHROE KEYWORDS VERSION ACCESSION DEFINITION SOCOL THILE JOUR**NAL** ORGANISM Advand AUTHORS Direct Submission Submitted (1: 197-200) National Institutes of Health, Mammalian Sens Collection (MCC), Cancer Genewics Office, National Cancer Institute, 31 Conter Drive, Room 11A03, Bethesdu, MD 20892-2590, NIH MAN Project TW. 11th /mgc not hib dow Contact. MMC help dcsk Email: cutpbs://mail.nih.dov Tissue Procurement: AICC BC001176 1992 Ep. SRNA linear PPI 12-701-2001 Bumo Sapions, transpokatamin II, Mactorylic anomia, olone MSC.2220 IMAGE:3353271, mkNA, complete cds. Eukarysia; Metacoa; Chordata; Craniata; Vertobrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1982) Strausberg, k Homo sapiens MGC. BC001176.1 GI:12654674 BC001176 human.

Result No.

Score Match Length DB ID

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SUMMARIES

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PEATURES
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Gocal Similarity 91.5%;
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Series: IRAL Plate: 6 Row: b Column: 1
This clone was selected for full length sequencing because it
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Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Sacedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Isai, Natasia van den Bosch, Jili Vardy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            passed the following selection criteria: matched mRNA g1: 339202
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Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Letticia Hsiao, Martin Krzywiński, Peta Kutsche, Glivet Lee, See
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CDNA Library Arrayed by: The L.M.A.C.E. Consettion (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Caneta Adency, Vancouvet, BC, Canada
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1167	gantanagannnaaggatggaggaaannattgagdtgaggdtggttagdtagddagddddi	1108	Оу	
1357	GAAAGSBAGTTCTGSCAGCTTCTCCGAGAGCCCCAACACCCCACTSTTGCAAGGTATTGCT	1298	Db	
1107	gaaagggagttetggcagetteteegagaeeeecaacaeeeeaetyttycaaggtattyct	1048	Qy	
1297	GAAACACAGGCCTCCTTGTCAGGCCCCTACTTAACCTTCCTCATGGGGAAAGCGGCCGGA	1238	Db	
1947	gaaácácaggeeteettyteaggeeeetaettaaceteeytyatyyyyaaayeggeegga	886	Qy	
1237	GCYSHSTICMACUSHISAAGATGTCTUSHSAAGAAGAAGACGCTTGAGTTAGGAGGATTCACATAT	1178	Dþ	
987	gccqgqtccaccqtggaagatgtcctgaagaaqqcccatqaqttaqqaqqattcacatat		Qy	
117	AGIGICACGCTGCAGGTGC IT AGICTCTTGCCGCCGTACAGACAGTCCATCTCTGTTCTG	1118	ф	
927	agtgtcacgctgcaggtgcttagtctcttgccqccqtacagacagtccatctctgttctg	858	Qy	
1117	GEACTACGACTICATEST (GGAACTAGCTGCTGAGACCATTCCTCAGACCCAAGAGATCATC	1058	ąg	
867	gcaccacqagtcatqttgqaaccagctgctgaqaccattcctcagacccaaqaqatcatc	808	Σ_{L}^{A}	
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                                                                                                        Clone distribution: MGC clone distribution intormation can be found through the 1 M A G F of secretium, TOM JC bett (The per 10d) are series: IAAK Flate: 19 Row: ) Column: 6 This clone was selected for full length sequencing because it passed the following selection criteria. Genomestan gene
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A.M., Holloway, M., Telford, B., Hoddson, A., Bonck, J., Yu, W.,
Muzny,D.M., Gibbs,R.A.
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Johnson, W.G. and Stenroos, E.Scott.
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Mammalla: Eutheria: Primates: Çatarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                    /note-"G00-119-608"
92. 1318
                                                                       /product="transcobalamin
                                                                                                                                                                                                                                                                                                                                                                                                                    QVLSLLPPYRQS ISVLAGSTVEDVLKKAHELJJGTTYETQASSSGPYLTSVMCKAAGEK
EEWQLLKDPNTPLLJGTADYRPKDGETTELRLVSW"
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TLAFCLUQKWYHDSVVDKFFYAVEFERQSHHSVDTAAMAGTAETDHKKSNENIGKRQR
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/product_Ttranscobalamin_II"
/protein_jd="AAA61054.l"
/db_xret_"GI:339196"
                                                                                                                   /evidence=experimental
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38. .1321
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/tissue_type "umbilical vein"
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/db_xref="taxon:9606"
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:AC 60	GTCCATGACAGCGTGGTGGACAAACTTCTGTATGCTGTGGAACCTTTCCACCAGGGCC	548
7GG 54	CACACTAGCTACTACCAGTATGGCCTGGGCATTCTGGCCCTGTGTCTCCACCAGAAGC	488
4.5		457
45	ctcaaatqqttcctqqqqqtqatqaqaaqaqaqccatt	421 428
ag 4:	geteteagageeaactytgagtit.gteaggggeeacaagggygaeaggeelqyteteae 	361 368
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                                                              CAG FICCICATGACTTCCCCCCACATGCGTGGGGCAGAACTGGGGAACAGCATGTCTCAAGGCG 863
                                                                          TTGAAGGCCAAACCCCCGAGGCCACTTTGGGAATGTCTACAGCACCCCATTGGCATTA 803
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ACCESSION

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Homo sapieus (clone V6) transcobalamin II (TCN2) m8NA, complete

1877 bp

mkna

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PRI 13-JAN-1995

VERSION KEYWORDS

binding protein; transcobalamin

II; transport protein

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/producto_id="AAAA61057 ;"
/db_xrvf "GI1339205"
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                                                                     Isolation and sequence analysis of variant forms of human
                                                                                                           and I.i.N.
                                                                                                                                             Seetharam, B., Arwert, F., Alpers, D. H., Lindermins, J., Sootharam, S.
                                                                                                                                                                                                                                                                                                   transcobalamin I
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GQLALVILALEANGEFVEGHKGDELVSQLKWELEDEKPALGHHKGHEHTSYYQYGLG
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/codon_star[1]
/roodon_transcobalamin_[1"
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Lissue Procurrement: Glibert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
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Contact. MGC help desk
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model. 10 month old virgin mouse. Taken by biopsy."
/clone_lib."NCJ_CGAP_Mam1"
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/db_xrof-"taxon-10090"
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 \Lambda \text{F121289}
Direct Submission
               2 (bases 1 to 1299)
Fedosov, S.N., Berglund, L., Nexu, E. and Petersen, T.E.
                                                                                     Fedosov,S.N., Herglund,L., Nexo,E. and Petersen,T.E. Sequence, S-S bridges, and spectra of lovine transcobalamin expressed in Pichia pastoris
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Submitted (20-MAR-1998) Department of Biochemistry, Medical College
of Wisconsin, MFRC Room 6061, 8701 Watertown Plank Road, Milwaukee,
WI 53226, USA
                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus
Eukaryota: Metamba: Chridata: Craniata; Vertebrata; Euteleestomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                               /strain "Sprague-Dawley"
/db_xref-"taxon:10116"
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EYWOLLHVPDTFLLGGIAGYRFK HEI ELIFILYKM"
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/protein_id "AAD55672.1"
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Whitehead Institute for Biomedical Research
9 Cambridge Center, Cambridge MA 02142 USA
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Fax: 617 252 1902
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Best Local Similarity 91.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             detines a metabolic or developmental process, treatment, condition, desage or disorder. The gene profile can be used for diagnosis, promosis or monitoring of treatments and for investigating a predisposition to a disorder where the gene is associated with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pharmaceutical adents. Expression of (I) in a sample indicates the differentiation of embryonic stem cells into a tissue selected from brain, heart, kidney, liver, lung, skeletal muscle or pancreatic tissues. (I) and (II) are used to produce an expression profile that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequences (1). (1) can have cytostatic, imbunomodulatory and noncoprotective activities, and can be used in gene therapy. (1) and proteins (11) encoded by then are used in high throughput screening
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Best Local Similarity
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                                                                                                                                                                                                                                                                          immunomedulatory, measural active general, voluntary, gastimintestina general; nephrotropic; antiinfective; gynecological; or antibacterial activity. The invention also includes antibodies specific for the
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Sequence 1299 BP; 269 A; 393 C;
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Best Local Similarity

19.6%;

Score 437; DB 22; Pred. No. 1. 4e-75;

Length 338

Query Match

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AAF68505/c
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95-WAF 2000: 2000US-0519642.
22-MAR-2000: 2000US-0534077.
10-AFR-2000: 2000US-0540259.
27-AFR-2000: 2000US-0560406.
95-JHN-2000: 2000US-0589184.
                                                                     to standard recombinant DNA methodology. Conversely, antisense NA molecules may be administed to down regulate protein expression. The Maind with the cells own genes and preventing their expression. The NA and complementary sequences may also be used as put probes in disquostic assays to detect and quantitate the presence of similar NA sequences in samples, and hence which patients may be in need of treatment for lung cancer. The (1) may be used as antiques in the production of antibodies and in assays to dentity of the protein. AAP68083 to AAP68878 and AAP68888 to AAP68888 represent human lung lumour protein related
                                                                                                                                                                                                                                                                  proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with their inappropriate expression, especially lung carcers. For example, the NAS may be administered to treat diseases by rectifying mutations or deletions in a patient's denome that affect the activity of the protein by expressing inactive proteins or to supplement the patients own production of (1). Additionally, the NAS may be used to produce the lung-tumour associated protein, according
                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes immonogenic portions of land tumour associated profeins (1) and the nucleic acids (NAs) that encode them.

(1) have cytustatic activity and can be used in gene therapy, antisense inhibition and in vaccines. The NAs and the lung tumour associated
                                  nucleotide and protein sequences which are used in the examplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lung tumor-associated proteins and the nucleic acids that encode them, useful for preventing, diagnosing and treating lung cancer.
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Sequence 338 BP; 68 A; 81 C; 117 G; 71 T; 1 other;
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17-DEC-1999;
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This invention describes novel human nucleic acid segments (1) containing polymorphic sites. The polymorled ides of (1) are used for, e.g. correlating disease proportions (or disease susceptibility) or other phenotypic traits (e.g. baldness, obesity, fortility, strength, response to drugs etc.); diagnosing and monitoring e.g. cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Piallolic marker polymorphism; busus; discuse; dialocsis; treatment; phenotypic trait; dene therapy; forensic; paternity; mapping; cancer; transaccio; ologic :scleatile polymorphism, SNP, as.
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                                                                                                                                                                                                                                                                                                Polymorphic human genomic sequences and related allele-specific probes and primers, useful tor genetic analysis, e.g. diagnosis and monitorine
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Torense analysis; quoe therapy; paternity testing; mapping genomic loci associated with phenotypic traits (and subsequent cloning of the genes responsible); and the production of transgenic organisms. Antibodies raised against (1) are useful as diagnostic and therapeutic books and in drag schooling, AdM85144—AAM87544 represent the human DNA sequences containing biallelie polymorphic sites described in the
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Fred. No. 1.9e-74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         containing polymorphic sites. The polymorleotides of (1) are used for, e.g. correlating disease polymorphisms (or disease susceptibility) or o bet phenotypic traits (e.g. baidness, obesity, fertility, strength, response to drugs etc.); diagnosing and monitoring e.g. cancer, intlammation, heart or central nervous system diseases detection susceptibility to microbial infection, treating or preventing such
How supiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           267
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                                                                              treatment; marker;
                                                                                                         autoimmune disease; cancer; inflammation; drug: therapy; medicament;
                                                                                                                                                detection; phenotypic typing; characteristic; infection; hereditary;
                                                                                                                                                                                   Polymorphism: biallelic; human; forensic; paternity testing; disease;
                                                                                                                                                                                                                                                              Human biallelic polymorphic DNA fragment WI-7281b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX11267 standard; DNA; 255 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibodies raised against (1) are useful as diagnostic and therapeutic tools and in drug screening. AAH85144 - AAH87644 represent the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 320; 330pp; English
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haemorrhagic telanglectasia, familial colonic polyposis, Bhlers-Danlos syndrome, estecapensis Experienta, acute intermittent porphyria, autosimune diseases, inflammation, cancer, diseases of the nervous system, inferien by pathogenic microcranisms, and characteristics such as longevity, appearance (e.g. baldness, obstity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid segments can also be used to produce medicaments for the treatment or products can also be used to produce medicaments for the treatment or products can also be used to produce medicaments for the treatment or products can also be used to produce medicaments.
                                                                                                                                                                                                                                                                                 can be used in methods for determining polymorphic forms in an individual for use in e.g. forensics, paternity testing or for phenotypic typing for diseases such as gammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy. Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterologia, polymystic kidney disease, hereditary spherocytosis, you willebrand's disease, tubercy sylerosis, hereditary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid somments from the human genome - used to
determining polymorphic forms for use in e.g. forensies, paternity
testing or phenotypic typing for disease
Sequence 255 BP; 53 A; 82 C; 70 G; 50 T; 0 other;
                                                 prophylaxis of such diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                        polymorphic markers which have been isolated using the primers represented in AAX09121-X10268. The base occupying the polymorphic site is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 138; 310pp; English.
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AAX11268
                       RESULT
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Best Local Similarity 100.0%;
Matches 255; Conservative (
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AAX11268 standard; DNA; 251 BP

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Best Local :
                                                                                                                                                                                       polymorphic markers which have been isolated using the primers represented in AAX°9[2] X1026 The base 52 49 in the polymorphic actual propersected by the appropriate TUPACTING ambiguity code. These trauments can be used in mathematics, patermining polymorphism for an infinite typing for discases such as agammaglobulinemia, disberses in spiritus, losen Myban syndram, muscular dystrophy, Wiskett Aldrich Syndrome, Edbry's disease, syndrome, muscular dystrophy, Wiskett Aldrich Syndrome, Edbry's disease, familial byporophism for losen a polymosis, hereditary spherocytosis, won Willbermand's disease tyberous schoresis, hereditary helmorphism telangication, tamilial colonic polymosis, Eblers-Danius hermands disease, those polymosis, Eblers-Danius
                                                                                                                                                                                                                                                                                                                                                                                                                       syndrome, osteogenesis imperfecta, acute intermittent porphyria, autoimmune diseases, inflammation, cancer, diseases of the nervous system infrestor by pathographic flores ranisms, and elacateristics such as longevity, appearance (e.g. beldiness, obesity), strength speed, endurance, fertility, and susceptibility or receptivity to particular drups or therapeutic treatments. The included polymorphic machain acid seminents of also be used to produce medicaments for the treatment or perceptivity or set acid.
                                                                                                                                                                                                                                                                                                                                                                      Sequence 251 BP: 53 A; 78 C; 70 C; 49 T; 1 other;
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1472 अवस्थान्यवर्षात्मा काम्युरात्मा वेषुष्ट्राप्तात्मात्रुव्वव्यवस्त्वतात्त्वात्त्रात्त्वात्त्वात्त्र्त्त् ।५४।
                                                                                                                                                                                                                                                                                                                                                                                                             prophylaxis of such discuses.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          determining polymorphic forms for use in e.g. forensies, paternity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid segments from the human genome
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                                                         Similarity
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99.68;
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                                                                                                                                                                                                                                                                                           Score 250.6;
Pred. No. 9e
                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                         9e-54;
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Matches 246; Query Match Best Local .

Conservative

14.3%; Score 245.4; DR 22; 99.2%; Pred. No. 1.96 52; calive c; Micmatches 2;

indels Length 256;

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Local Similarity

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                                                        mimetime, peptides, proteins, agonists, antagonists, antibodies or their transcats, immunositudies, inhibitute, dies emporads and pharmacentical agents. Expression of (1) in a sample indicates the differentiation of embryonic stem cells into a tissue selected from train, heart, kidney, liver lung, skeletal pusche or paperatic tissues. (1) and (11) are used to produce an expression profile that derines a metabolic or developmental process, treatment, condition, disease or disorder. The gene profile can be used for diagnosis, it desires a mentacring of treatments and for investigating a predisposition to a disorder where the gene is associated with a
                                                                                                                                                                                                                                                                    AAH57161 to AAH57576 represent cell and tissue specific polynucleotide so precies (1). (1) can have sytostatic, terminomobiliatory and neuroprotective activities, and can be used in grow therapy. (1) and proteins (11) encoded by them are used in high throughput screening assays to sole, t DNA molecules, RNA molecules, poptide nucleic acids,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Now coll and dissue specific polynucleotides useful for diagnosis, prognosis of monitoring of treatments for disorders where the gene is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lung: liver; vterus: evary; stomach; intestine; kidney; pasgreas; ss;
metabolic discuse; developmental discuse; sytostatic, immonomodulatory;
nearoprotective; gene therap; cancer, immonopathology, nearopathology;
Serguence
                                           dalidet,
                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 121; 327pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human kidney specific cDNA sequence SEQ ID NO:147
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                                                                                                                                                                                                                                                                                                                                                                                                                                        associated with a cancer, immunopathology or neuropathology
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                                       immunopathology of neuropathology.
  256 BP; 55 A; 86 C; 62 G; 52 T; 1 other;
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\overset{\times}{\times}\overset{\times}{\overset{\times}{\times}}\overset{\times}{\times}
                                                                                                                                                                    mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and generic DNAs. 5' ESTs are also used in diagnostic, forensic, generic therapy and chromosom mapping procedures. They are used to obtain generic therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. An ORP has been identified within the sequence. The 5' ESTs were prepared from total brand PNAs or polyA- PNAs derived from 40 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTP) of the mPNA because they are
                                                                                                                                                                                                                                                                                                                                                                                                                 often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5^\prime ends of
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Best Local Similarity

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Score 201.8; D8 2 Pred. No. 2.4e-41;

DB 21; Length 377;

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                                mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or by At RNAs derived from 30 different tissues (ST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from objected region (WTR) of the mRNA because they are often obtained from objected RNA libraries. Such ESIs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESIs are derived from mRNAs with intact 5' ends and such therefore be used to obtain tall length constant and genomic DNAs. 5' ESTs are also used in diagnostic, foreusic, gene therapy and chromosome mapping procedures. They are used to obtain sections are tall according to the section of some obtain and procedures.
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                  upstream regulatory sequences and to design expression and secretion
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                                                                                                                The inverties relates to a single each buckle acid probe for measuring human dene expression in a sample derived from human toolad liver. The single even medicinate forber may be used for predicting measuring and displaying gone expression in samples derived from human fetal liver. The present sequence is a single exem nucleic acid.
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08-Auto-jouro- 200009 08-49-46
21-8EP-2000; 200009 0294687,
27-8EP-juno- 200009 024686
04-007-2000- 20000P 0624263
Note: The sequence data for this patent did not form part of printed specification, but was obtained in electronic format from WIPO at ttp.wipo.int/p.b/p.bliskd_pct_Sequences.
                                                                 probe of the invention.
Note: The sequence data
                                                                                                                                                                                                                                                                                                                                                               Human geneme-derived single exon nacleic acid probes useful analyzing gene expression in human tetal liver
                                                                                                                                                                                                                                                                                                   Claim 1; SEO 1D NO 12642; 639pp · sequence listing; English
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26-MAY-2000: 200005-0207456
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27 SEP-2000; 2000US-0236359
04-001-2000; 2000GH-0024263
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F MAY-2000;
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                                                                                                                                                                     The present insention relates to single each nucleic acid probes for
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                                                                                                                                                                                                                                                                                                                     Simple exon medete acid probes for analysing dene expression in human
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vascular disease; bypertension; cardiac arrhythmia;
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2000US-0207456
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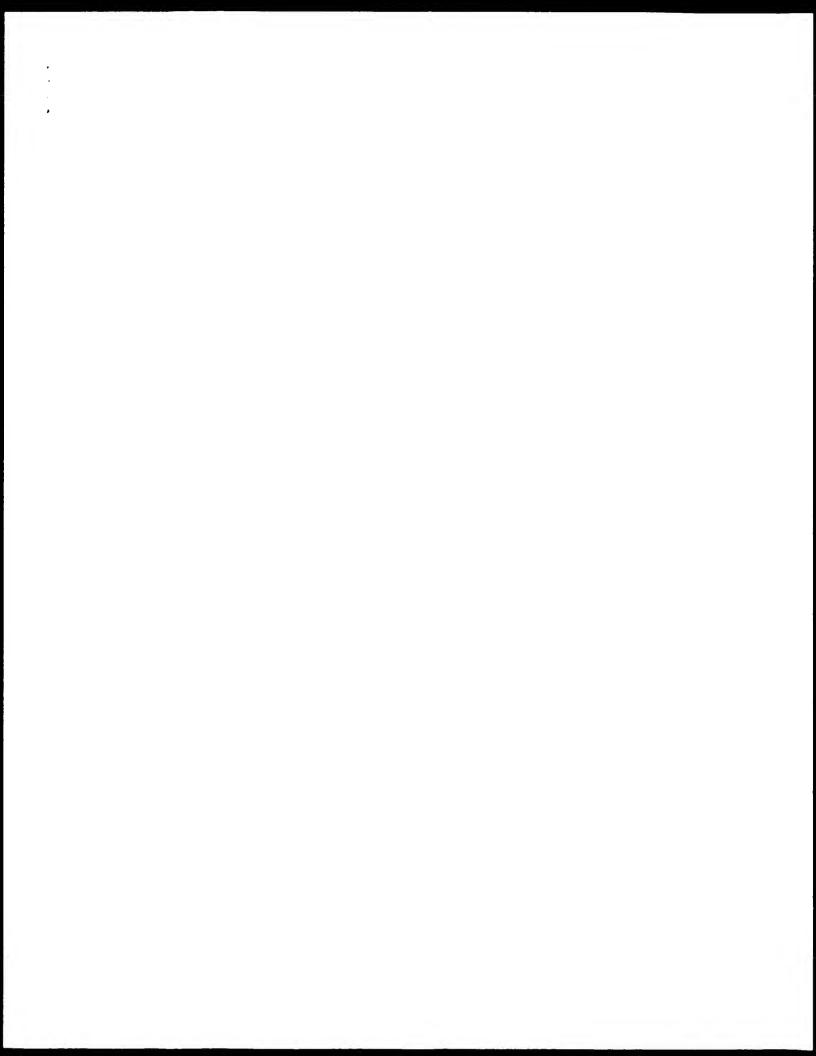
present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the bunar heart via microarrays, by measuring and displaying gene expression in samples derived from the bunar heart via microarrays, by measuring accomplession, the probes are useful for predicting, diagnosing, grading, staging,

monitoring and prognosing diseases of the

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21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                    21 SEP-2000; 2000US-0234687.
27 SEP-2000; 2000US-0236359;
04-03T-2000; 2000GB-0024263.
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probes which are derived from genomic sequences expressed in the human
                                                   Example 4, SEQ ID NO: 12792; 650pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                  04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200157275-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; brain expressed exon, gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-NoV-2001 (tirst entry)
               The present invention provides a number of single exon nucleic acid
                                                                                                             Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                         WPI; 2001-483446/52.
                                                                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                  30 · JUN - 2000;
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Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKE2), Email s wiemann@AKF- heidelberg.de;
segmented by GPE (Mariana) Fissaarch Centur for Bistechnology Itd.,
bisaanschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
It sequence also available.
This close available is available, the EDPS in Berlin.
Hease available the kEFD: Ressourcensentium, Heabherweg b, 14059
Berlin Charlottenkary, GERMANY, Fmail elementy.
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Contact: Bloecker H
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/db_xrof-"haxon 9606"
/clone_lbFsp434H1915"
/clone_lbF-434 (synonym: htes3)"
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/dev_stage="adult"
/lab_host="DH10B"
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1 (bases 1 to 772)
NCL/NINDS-CGAP http://www.ncbi.nim.nih.gov/ncicgap
National Cancer Institute / National Institute of 
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Email: egaphs romail.him.gav
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/tissue_type="glioblastoma (pooled)"
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cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution NCT-GGAP close distribution information one po-
found through the LLM A.G.E. Consortium/LLNL at:
www.bio.llm.jou.lbrg.Teap.Teap.html
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wp74468 xl N61 69AP Rines Home sapiens e5NA ejece (MAGE-246767) 3
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National Cancer Institute / National Institute of Neurol
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                                                                                                     Library is normalized, and was constructed by Best. Sources and McFatima Honaldo " 189 c 227 g 153 t 4 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCT-CGAP http://www.ncbi_nlm_rib_gov/ncicgap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       www-bio.llnl.gov/bbrp/image/image_html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          found through the L.M.A.G E Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type "adenocarcinoma"
/lab_host "DH10B"
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                                                                                                                         wg43e96.xi Soures_NSE_F8_9W_0I_FA_F_Si Homo sapiens cDNA clone tMAGE:J367891 31 similar to qb:L0J648 [RANSCHBALAMIN]] I FRECTROUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: egapbs-rémail.nih.gov
This clone is available revalty-tree through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 649)
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A1742486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the same 5 libraries. The pools consisted of the following libraries and clonelps: Scares wbHSF pool 1: 309384 310919, 373008 375005 SSATES WbHPP pool 1: 45032 147306, 147720-14810, 14872-14925, 35092-150407, 151176-152327 Soares WbHPP-9001 1: 758260-750595, 772104-774407 Soares WbHPP-901 1: 758260-750595, 772104-774407 Soares WbHPP-901 1: 758260-750595, 772104-774407 Soares WbHPP-901 1: 75820-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 30470-750505, 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a subtractive hybridization reaction. The driver was {\rm ECP-3mpiified~clnAs} from {\rm ECP-3mpiified~clnAs} from
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/clone="IMAGB:2367874"
/clone="tib-"S-ares_NSF_FR_9W_OT_PA_P_S1"
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Tissue Procurement: ATCC
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/tissue_type="adrenal cortex carcinoma, cell line"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1997)
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Contact: Robert St:
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WHI MAR http://www.nebi.nlm.cib.journeingap
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40UP from Gibco
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Mammalia: Euthoria. Primates. Cafaribini. Hominidae: Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.cih.gov
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/lab_host-"DH16R"
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libraries were mixed, and ss circles were made in vitro.
Following HAP purification, this DNA was used as tracer in
a subtractive hybridization reaction. The driver was
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                                                                                                                                                                                                                                                                                                                                                                  1353 ccaaqcatcttccctqqqaaqtctttctqqccaaqtctqqccaqqcttqqccqqqtc 1412
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1 (bases 1 to 587)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,B., Lennon,G., Marra,M., Martin, M., Monte,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapieus
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This clone is available royalty free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq.primer: -41m13 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WashU-Merck EST Project 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified chNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of L.M.A.G.E. clones 262232-265223, 340488-345479, and 484488-489479.
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prognant uterus"
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/db_xret="taxon=9606"
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Pred. No. 7.3e 72;
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 518 bp mRNA linear EST 30-MAR: nab66c02.x1 Soares_NSF_F8_9W_0T_PA_P_S1 Homo sapiens cDNA clone iMAGE: 3272810 37, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This cione is available royalty free through LLML; contact the IMAGE Consortium (into simage.linl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                     Following HAP parification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCP-umplified cPNAs from pools of 5,000 closes made from the same 5 libraries. The pools consisted of the following libraries and closelys Soares NBHSF pool 1: 309384:310919, 323208:335895 Soares NBHSF pool 1: 309384:310919, 323208:335895 Soares NBHSF pool 1: 145032:447385, 147720:448109, 148872:149255, 15092:-150407, 151176-152327 Soares NBBF8-9W pool 1: 252280-350584, 772194-774497 Soares NBBF8, pool 1: 304776-30584, 320136-332823, 345280-326663 Soares NBHOT pool 1: 723720 736407, 739080-740999 Subtraction by Bento Soares and M. Fatima Bonaldo."
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                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: pooled; Vector: pT7780-Fac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; Egual amounts of plasmid DNA from live normalized libraries were mixed, and ss circles were made in vitro.
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/clone="IMAGE:3272810"
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r∘mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: Fite Technologies, Inc. cDNA Library Arrayed by: Groy Komenn, FL.P. Chan Library Arrayed by: Groy Komenn, FL.P. Chan Sequencing by: Muskington University Genome Sequencing Notice Clone distribution: NCT-CGAP clone distribution information can be found through the L.M.A G E. Consertium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCI-CGAP bitp://www.mcbi.nlm.mib.gov/noicgap.
Mational Capser Institute, Capser Cepter Anatomy Project
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/db_crot "taxos 3606"
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                                                                   Eukaryola: Metazoa; Chordata; Craniata; Vertebrata, Euteloostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 594) Hillier: Alies, M. Rowles: L. Hoberpar, J. Goisel, G., Lost, S.,
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//Soft "Fight Stownich, Verbut PCMV-SPORT6; Site_1: Salt; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.69 kb life Technologies catalog #: 11549-011"
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93.8%; Pred. No. 8.50-69;
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                             1501 gaagaCoactcqffctgtqqttggggteetgeaaqaaqtootceteagoocygyggggat 1969
                                                                                                                                       | 1461 | NAGCATGAGAG ALCTGAGAGCT (2017) | 2500 | 251 | 251 | 252 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 | 253 |
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                                                                                                      420 GGGCATGAAGCATCTCAGAATCCTTGGCAAAAAAGGGAGTCCGCAGGCCGCAGGTGTTGT 479
                                                                                                                                                                                                                                                                                                                                                                                             300 CCCTATACCATGGCCCACCTTGGAGCAGGAGGCAAGCATCTTCCCTGGGAAGTCTTTCT 359
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                                                                                                                                                                                                                                                  GROTAAGTOTOROTAGOCTGGGAGTGCAGGTGTGOTATTAAGGTOTATTGGTOTGAT 41 4
Email: est-watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Comsortium (info@image.lini.gov) for further information
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 211.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      was used as tracer in a subtractive hybridization reaction. The driver was PCK amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 1 M A C.F. clones 26023, 265223, 340488-345479, and 484488-489479.**

1. 169 c. 162 g. 129 t. 1 others
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Sucry Match 27.30, Store 480.2, U6 5, Length 502; Best Local Similarity 97.48; Pred. No. 2.46564; Matches 498; Conservative O; Mismatches 13; Indels O
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Contact: Robert Strausberg, Ph.D.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 10.1%; Score 286.8; DB 10; Length 584; Socal Similarity 98.7%; Pred. No. 1.4e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 CCGGTTCTACTCCTTGTCCTGGGCAGCAGGGGCACTACCA-GGGCTCCTTTGGTAAGGAG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGENOG FOGACAGACI IGACAGA LOAGGCATCAGUCCCTCTGCGCTGGTCCCGGGCT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Please contact the RZFO: Ressourcenzentrum, Heubnerweg 5, 14059
Berlin:Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                       Am Klopterspits 18a D 82152 Martinsried, Sermany
This is the 5' sequence of the close insert
Close from S. Wiemann, Molecular Jevene Analysis, German Cancer
Resourch Center (DKFZ): Email s.wiemann-dkfz heidelbord.de;
Sequenced by ACCWA (Herlin/Sermany) within the CDNA sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Contact: Wambutt R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DKF2p0s600316_ri b8b (synonym: hlee3) Homo sapiens cDNA clone DKF2p08600416 5%, mkNA sequence.
                                                                                                                                                                                                                                                                                                                                          consortium of the German Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST (Wambutt, R., Heubner, D., Mewes, H.W., Weil, B. and Wiemann, S.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wambutt, R., Heubner, D., Mewes, W., Weil, B. and Wiemann, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                             This clone (DKFZp68600316) is available at the RZPD in Berlin
                                                                                                                                                                                                                                                                                                                      No si sequence available.
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                 /note "Vector, pTriplEx2, Site_1. SfilA; Site_2: Sfilb cDNA-collection"
                                                                               /lab_host ."DH10B"
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                                                                                                                                                                                       ∕orqanism "Homo sapiens"
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Best Local Similarity 96.9%;
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1 (bases 1 to 443)

Billier, L., Lennon, G., Becker, M., Honaldo, M.F., Chiapelli, B.,

Chissoe, S., Dietrich, N., DuBuque, T., Favelia, A., Gish, W., Hawkins

Chissoe, S., Dietrich, N., DuBuque, T., Favelia, A., Gish, W., Hawkins

M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Morris, M., Parsons, J., Pranago C., Kitkin, L., Kobilling, T.,

Schellenberg, K., Svares, M. B., Ban, F., Thiorry-Man, L., Thamskis, E.,

Underwood, K., Wohldmann, P., Waterston, R., Wilson, F. and Marra, M.,

Generation and analysis of 280,000 human expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA171576 443 bp mkNA linear EST 2+-DEC 199 zp23a05.rl Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:610256 5' similar to qb:L02648 TRANSCOHALAMIN II
                                                                                                                                                                                                                                                                                                                                  IMAGE Consortium (into*image.lini.gov) for further information. Seq primer: .28M13 rev2 from Amersham High quality sequence stop: 356. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Wilson kK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97044478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4444 Forest Park Parkway, Box 9551, St. Louis, Mo 64108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metagoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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         Actions "IMAGE, 50-256"
Actions it "stratagens in an application (#267241)"
Ader_stage "Hiera 2,78A include the limit (#267241)"
Ader_stage "Hiera 2,78A include the limit (#268")"
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                                                                                                                                                                                                           /db_xref-"taxon:9606"
ceils (Ntera 2/cl.Dl) induced with Retinoic Acid for 24
                                                                                                                                                                                                                                           /organism:"Homo sapiens"
/db_xret:"GDB:4625515"
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Pred. No. 2e-41;
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Mammalia: Eutheria: Primates: Catarrhini; Hominidae; Homo.
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                  /hissw_type Hamma, /
/hote "Vector: pME188123"
/hote "Vector: pME188123"
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a 261 c 238 g 181 t
                                                                                                                                                                             /db_xret="taxon:9606"
/cione="MAMMA1002885"
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Insert Length: 571 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be tound through the L.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Emmert Buck, M.D., Ph.D. cDNA Library Preparation: David B. Krizman, Ph.D. cDNA Library Arrayed by: Greatennon, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cyapbs-r@mail.nih.gov
Tissue Procurement: L. Jeffre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOI-CGAP littp://www.prbi.plm.pih.gov/pologap
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
l (bases l to 366)
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                                                                                                                                                                                                                  /note "Vector: pAMP[0; mRNA made from liposarcoma, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 l Reference: Krizman et al. (1996) Cancer Research 56:5480-5383."
                                                                                                                                                                                                                                                                                                                                       /tissue_type="liposarcoma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                   /clone "IMAGE:1061463"
/Clone_116 "MFI_CCAF_61p2"
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HS_5571_B2_502_F7A RPCF-11 Human Maic BAC Library Homo sapiens
genomic clone Plate-1147 Col-4 Row H, DNA sequence.
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Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                http://www.htsc.washington.edu
Plate: 1147 row: H column: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                     gAliA. Research Genetics (into reston, com). HAY and Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clones are derived from the human RA. Hibrary RG-1-11, For RA. Hibrary availability, please contact Pieter de Jouq (Pieter de)cont.med.but algo, edu). Cheese may be purchased from RA.T.A. Researches (117) Bergar med Hotto:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High Throughput Sequencing Center
University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Mahairus GG, Wallace JC, Hood L
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Froc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
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Mahairas, G.G., wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: jwallacemu.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40] Queen Anne Avenue North, Seattle, WA 98109, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D.
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                    Zhate "Vector, pBANGLA, Site_1. Keekl, Site_1. Bookla
Male blood DNA was isolated from one randomly chosen domor
and partially disperted with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was closed into the
pBACe3.6 vector at Ecokl sites"
                                                                                                                                    /sex="male"
                                                                                                                                                                                                                    /organism "Homo sapiens"
/db_x:et "taxon:9606"
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The Institute for Genomic Research
9712 Medical Conter Dr., Rockville, Mr 20850, USA
Tol: 391 848 3528
Fax: 301 838 0208
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The Institute for Genomic Research
9712 Medical Center by Ferweille, MD 20850, USA
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AL601711
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This is the 5' sequence of the clone insert
Those from 5' McCompan, Molecular Genome Analysis, German Cancer
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Mammalia, Eutheria, Primates; Catarrhini, Hominidae; Homo.
1 (bases 1 to 713)
                                                                                                                                                                                                                                                       Berlin- Charlottenburg, GERMANY; Email: clone⊌rzpd.de
                                                                                                                                                                                                                                                                                                                     available.
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                                   /lab_host="DH10H"
/note="Vector: pTriplEx2; Site_1: SfilA; Site_2: SfilH; cDNA-collection"
                                                                                               /clone="DKF5p313A247"
/clone_lib="313 (synonym: hlec2)"
/dev_stage="adult"
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Other_GSSs: RPC[]11-270]3 TV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             library hmillability, please contact Pieter de Jong (pieterädejong med buffalo.edu). Clones may be purchiased from BACEAC besteroes (litp://barpar med buffalo edu/orbing) or from Research Genetics (info@resgen_com). RAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mdadams@tigr.org
Clones are derived from the human BAC_library RPCI-11. For BAC
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/clone="kPCI-11-27013"
/clone_lib="RPCI-11"
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HS_3096_Al_E01_MF CIT Approved Human Genomic Sperm Library D Homo
Saprens yearoutt trane Plate-Auge Col-1 Row-T, DNA sequence.
                                                                                                                                                                                                                                                                         401 Queen Anne Avenué North. Seattle, inc. (766) 616-38878
Fax: (206) 616-3897 Fmail jwallar-a washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 482)
Mahairas, 9.6., Wallace, 1.C., Smith.K., Swartzell.S.,
Keilt, A., Shaker, F., Fitledg.J., Young.J., Thoo, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                        99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                           scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739 9744 (1999)
                                                                                                                                                                                    High quality sequence stor, 482
                                                                                                                                                                                                           Class: BAC ends
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                                                                                                                                                                                                                                                                                                                                                                High Throughput Sequencing Center
University of Washington
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Mammalia, Eutheria, Frimates, Catarrhini. Hominidae, Homo.
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70; Conservative
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a 127 c 134 g 147 t
                     'sex-"male"
                                        /db_xrcf "taxon:9606"
/clone="Plate=3096 Col-1 Row-I"
/clone_lib="CIT Approved Human Genemic Sporm Library P"
,hoto "Ergan, Sporm, Vestor, pholobactl, had Clones
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480
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   Pred. No. 4.2e-28;
   O. Mismatches 79, Indels 5;
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                                                                                                                                                                                                                                      Submitted (02-AUS-2001) Asia Fujiyama, The Institute of Physical and Chemical Research (RIXEN), Genomic Sciences Center (GSC); I-7-22 Suchiro chou, Tsuremi ku, Yokohama, Kanagawa 230-0945, Japan (b-muil crimiphes Bestiketies); GRL http://hyp.gso-irket-respectiveles: B1-45-503-9111, Fax:Ki-45-503-9120, Clones are derived from the chimpances and library RPCI-43 This BAC Clones are derived from the chimpances and library RPCI-43 This BAC Clones
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Par troplodytes male lymphocytes PNA, close_lib.RPCI-43 Chimpannee
Male BAC Library close:RP43 022L02.T7.
                                                                                                                                                                                                                      end was demorated during the ESP process and may have higher
                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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Fotoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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Totoki,Y., Watanahe.H. and Sakaki,Y.
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Best Local Similarity 80.0%;
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Clones are derived from the chimpanzee BAC library PIB This BAN end
                                                                                                                                                                                                                                                                                                                                                                                                                                             GSS; GSS (genome survey sequence).
Pun trogledytes male lymphoblast DNA, clone_Hib:PTB Chimpanzoo Malo
BAC Library_clone:PTB-030N18.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fig. troglodytes DNA, clone: FTR-030K18.R, denomic survey sequence AC950432
                                      clone tracking errors.
                                                           was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                          Fujiyama,A.,
Totoki,Y., W
                                                                                                                                                                                                                                                                                   Unpublished
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Totoki,Y., Watanabe,H. and Sakaki,Y.
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Sequencing: M13Rev
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/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
                                                                                                                                                                                                                            , Watanabe, H. and Sakaki, Y.
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                                                                                                                                                                                                                                               Hattori, M., Toyoda, A., Tayler, T.b., Yada, T.,
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Query Match 7.3%; Score 206.2; DB 12; Length 664; Best Local Similarity 76.0%; Pred. No. 7.40-28; Matches 273; Conservative 0; Mismatches 73; Indels 13; Gaps
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acute myeloid leukaemia; Altheimmer's disease; Albs; epilepsy;
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rhoundatoid arthritis, psoriasis and inflammatory/dicerative bowel diseases. The present sequence is a gene of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     manular degeneration, arterioscherosis, anaemia, cancer, acute myeloid
leukaemia, Alzheimor's disease, AluS, epilepsy, neurofibromatosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, necosacular glaucoma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid comprising tragment of chemically modified gene, useful to filagnosis and treatment of discases associated with abnormal
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Hest Local Similarity
Matches 1991, October
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antificitammatory; cancer; eye disease, arterioseterosis, anae
aeuto myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8577 BP; 1955 A; 128 C; 2062 C; 4432 T; 0 other:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and
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analyzing gene expression in human fetal liver
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Query Match
                                                                                                                                                                                                                                                                     The present invention relates to simple exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for
                                                                                                                                                                                   e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
                                                                                                                                                                                                   monitoring and prognosing diseases of the buman breat and vascular system
                                                                                                                                                                                                                   predicting, measuring and displaying one expression in samples derived
from the human heart via microarrays. By measuring one expression, the
probes are useful for predicting, diagnosing, grading, stading,
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26 MAY 2000;
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27-SEP-2000;
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30-JUN-2000; 2000US-0608408.
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                                                                              Semplement 569 BP; 162 A; 126 C; 153 C; 128 T; 0 other;
                                                                                                                                 specification, but was obtained in electronic format
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Matches 569;

Conservative

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26-MAY-2000;
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microarray: Alabelmor's disease, multiple selectsis, achicoph
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                      AAK 38101
                                          RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides a number of single exon nucleic acid probes which are derived from decomic sequences expressed in the human brain. They can be used to measure gene expression in brain vell samples, alc. Language to the draft. Since our improved to the terminal system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 569 BP; 162 A; 126 C; 153 G; 128 T; 0 other;
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AAK98101 standard; DNA; 569
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Human bone marrow expressed single exch probe SEQ ID NO: 12658.

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Best Local Similarity
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100.0%; Prod No 2 %-120;
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Query Match Best Local Similarity Matches 569; Conserv

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                                                              expression, the probes are therefore useful in quading and/or stading of discases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed
                                                                                                                  The present invention relates to human simple exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical critical cells. By measuring gene
                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JUN-2000; 2000US-0608408

93-AUC-2000; 2000US-0632366

21 SEP 2000; 2000US-0234687

27-SEP-2009; 2000US-0236359
                               specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human pervical epithelial cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-PES-2000; 2000US-0180312
26-MAY 2000: 2000US 0207456
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Sequence 569 BP; 162 A; 126 C; 153 G; 128 T; 0 other;
                                                                                                                                                                                                                           Claim 25; SEQ ID No 8808; 487pp; English.
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21-SEP-2000; 2000US-0234587.

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Matches 412; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disease or disorder. The wene profile can be used for diagnosis, prognosis or monitoring of treatments and for investigating a prodisposition to a disorder where the gene is associated with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             minedies, peptides, proteins, agonists, antagonists, antibodies or their fraqments, immunoglobulins, inhibitors, drug compounds and pharmaceutical agents. Expression of (1) in a sample indicates the differentiation of embryonic stem cells into a tissue selected from brain, heart, kidney, liver, lung, skelentel muscle or pancreatic tissues. (1) and (1i) are used to produce an expression profile that decines a metabolic of device produce and expression profile that the state of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the second product of the
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Query Match 9 1%;
Best Local Similarity 99.2%;
                                                                                                                                                                immufrom adulatory. Easilar antipolagore and witherary, gastrining that general, nephrotropic, antiinfective, gynecological; or antibacterial activity. The invention also includes antibodies specific for the protein or polynucleotide sequences. The lung cancer associated polynucleotide sequences may be used for detection of lung cancer, chromosome identification, as chromosome arkers, and for numerous other dispression or research purposes. The proteins may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders. The proteins may also be used in the treatment of wounds and infractions dispasses. Polynumberable sequences AAF18425 - AAF1843 and peptide AAB36549 are used in the course of the invention for the identification.
                                                                                                                                                                                                                                                                                                                                                                                                                            Polynucleotide sequences AAF17982—AAF18424 encode human lund cancer associated proteins represented in AAB58106 · AAB58548. Lung cancer associated proteins and polynucleotide sequences, their aqunists, and antagonists may have neuroprotective; cytostatic; cardioactive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lung cancer associated gene sequences, referred to as lung cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as lung cancer –
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cardioactive, immunomodulatory, magular active; yelecatery;
gastrointestimal, nephrotropie, antilifective; synecological;
antibacterial; diagnosis; neural disorder; immune disorder; reproductive;
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                                                                                      Sequence 1299 BF; 269 A, 393 C,
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(HUSE/) FOSEN C A
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MO 63108, USA
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Submitted (19-AUG-1999) Department of Genetics, Washington University, 4444 Pagest Park Avenue, St. Louis, Missouri 63108, 7 (bases 1 to 101720)
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Direct Submission
Submitted (03-101-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
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Human chromosome 14 DNA sequence BAC R-75014 of library RPCI-11
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] (bases 1 to 183672)

Rollid,R., Petit,J.L., Vico,V., Dasilva,G., Robert,C., Wincker,P., Brottler,P., Cattolizo,L., Barbe,V., Pellotier,P., Artionenave,F., Levy,M., Eckenberg,R., Brulls,T., deBerardinis,V., Cruaud,C., Gyapay,G., Saurin,W. and Weissenbach,J.

Sequencing of the human chromosome 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - Web - www genoscope.cns.fr)
On May 2, 2001 this sequence reraice replaced gi:10280510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The following BAC sequence is oriented from the T7 to the SP6 end Upstream BAC (overlapping the T7 end): R-951P22 townstream BAC (overlapping the SP6 end): R-439132 (AC AL161662)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.genoscope.cus.fr/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center gode: GS
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BF 191 91006 EVRY cedex - FRANCE (Fomai) - segref-genoscope.cus.fr
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                                          Identified using the e-PCR software (G. Schuler)", 39946 c. 43028 q. 51670 t
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Human chromosome 14 DNA sequence MAC 8-439L12 of library RDCI-11
from chromosome 14 of Homo sapiens (Human), complete sequence.
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                                                                                                     Center: Genoscope / Centre National de Sequencage
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BP 191-91006 EVRY dedox - FRANCE (Ermail : Segret@genoscope.cms.fr
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Mammalia: Entheria: Primates: Catarrhini: Hominidae: Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Center code: GS
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www.qenoscope.ons.fr)
...-- Genome Center
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Pred. Ro. 1.76 57,
0, Mismatches 78; Indels 0; 0
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FEATURES
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Hest Local Similarity 78.5%; Pred. No. 1.8e-57;
Matches 284; Conservative 0; Mismatches 78
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Location/Qualitiers
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44
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kHdb.kH76454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dbsTs:sIs68248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RHdb: RH98490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identified using the e PCR software (G. Schuler)" 131576. .131767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Klidb: KH53896
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/clone_lib "RPCI-11"
8/848
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∕chromosome-"14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"matching EMBL:AA477§24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         identified using the e-PCR software (G. schuler)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"matching EMBL:H61739
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Linton, E., Nosbaum, C., Tander, E., Allen, N., Anderson, M., Baker, J., Baldwin, J., Barna, N., Beckerly, F., Penn, J., Rrown, A., Castle, A., Cerny, J., Galangela, M., Collins, S., Callymore, A., Cooke, P., DeAtellano, K., Depayre, E., Devon, K., Dewal, K., Porcelan, L., Deyle, M., Perreita, P., Fitzhugh, W., Porrest, C., Funko, P., Gade, D., Galagan, J., Gardyna, S., Gilbert, D., Grant, G., Hados, B., Heaford, A., Horton, L., Howiand, J. C., Joues, C., Kanatas, A., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, H., McCasta, A., McKennah, K., McLaughlin, J., Molla, M., Morris, W., Morrow, J., McDaughlin, J., Molla, M., Morris, W., Morrow, J., Mychalecky, J., Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Pavlin, B., Peterson, K., Follara, V., Eiley, E., Esberts, D., Egy, A., Severy, P., Stanger-Thomann, N., Stoljanovic, N.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCO07780 166205 bp DNA Linear HIG 06 JAH 20
Homo Supicus chromosome 17 ctone CTD-2004N4 map 17, WORKING DRAFT
                                                                                                                                                                                                                                       * NOTE: This is a 'working draft' sequence. It currently * consists of 6 contigs. The true order of the pieces * is not known and their order in this sequence record is * arbitrary daps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On Dec 22, 2001 this sequence version replaced All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (199-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
2 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://ftp.genome.washington.edu/kM/KepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Research, 320 Charles Street, Cambridge, MA 02141, USA On Dec 22, 2001 this sequence persion replaced violegy4274.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (10-JUN-1999) Whitehead Institute/MIT Center for Genume
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC007789.7 G1:17977451
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                                                                                                                                                     be preserved.
                                                                                                                                                                                              as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 166205)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 166205)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insert size, 160000, agarose fp
Insert size, 165705, sum of contigs
Quality coverage: 16.3 in 020 base.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Consensus quality: 164894 bases at least 248 Consensus quality: 165452 bases at least 230 Consensus quality: 165602 bases at least 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: Plasmid; n/a; 71% of reads
Chemistry: Dye primer amersham; 24% of reads
Chemistry: Dye-terminator Big Dye; 76% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: L887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Assembly program: Phrap; version 0.960731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center code: WIBR
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846 945: gap of 100 bp
946 1944: contig of 999 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Center
                                                                                                 845: contig of 845 bp in length
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DEFINITION

AC099684

Homo sapiens chromosome 17 clone CTD-2545H1 map 17, WORKING DRAFT

191887 bp

UKA A

linear

HTG 18-NOV-2001

AC099684

VERSION KEYWORDS

HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP

SEQUENCE, 28 unordered pieces. AC099684 AC099684 1 GI:16974138

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                                                ph 130694 TTTT 130691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPIGIN
                                                                                                                                                                                                                                                                                                                         Db. 130934 CCTACCTCAGTCTCCCAAGTAGCTGGGATTACAGGTGTGTGCCACCACGCTCAGCTAATT. 130875
RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 8.3%,
Best Local Similarity 79.7%;
Matches 290, Conservative
                                                                                  1279 ttgt 1282
                                                                                                                                                                                                                                                                                                                                          1040 cctgcctcagcccccaagtagctaggattacagacgtctqccaccacgccaggctaati 1099
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2045 10326: contig of 8282 bp in length
10327 10426: gap of 100 bp
10427 24737: contig of 14311 bp in length
24738 24837: gap of 100 bp
24838 48541: contig of 23704 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48542 48641: gap of 100 bp
48642 166205: contig of 117564 bp in length
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24838. .48541
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19427. .24737
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contin of 23704 bp in length
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Fatta, N., Bastlen, V., Beyaslaviy, L., Boskhqalter, B., Brown, A., Camarata, J., Campopianto, A., Chanq, J., Chazato, B., Choopel, Y., Colanqalo, M., Collins, S., Collympic, A., Cook, A., Clook, P., Follandelo, M., Collins, S., Collympic, A., Cook, A., Cook, P., Fattiston, K., Foreira, K., Fattiston, K., Foreira, P., FiltzHugh, W., Gage, D., Galagan, J., Gardons, S., Goyette, M., Graham, L., Grand-Pierro, N., Hagos, B., Heatord, A., Horton, L., Hulmo, W., Iliev, L., Johnson, R., Toope, S., Gage, D., Galago, J., Gardon, R., Johnson, R., Foreira, P., Galago, J., Gardon, J., Gardon, R., Johnson, R., Filton, J., Gardon, J., Johnson, R., Johnson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          * NOTE: This is a 'working draft' sequence. It currently * consists of 20 mostigs. The true order of the plymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smit, A.F.A. & Green, P. http://rg.ho.com.astling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        All repeats were identified using hepcatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sabedith-4 (18-NOV-2001) Wilhobert Postitute/Hil Contr
Research, 420 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 inoun, J., Sembek, L., Simmer, A. and Sody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jones C. Kamat, A. Karatas, A., Kells, C., LaRocque, K.,
Lamazares, R., Landers, T., Lehocky, J., Levine, R., Liu, G.,
MacCean, C., Macdonald, P., Major, L., Marquis, N., Matthews, C.,
McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Moldrim,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 17, clone CID-2545H]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota: Motacoa: Chordata: C:aniata; Vertebrata: Extelesistomi;
Mammalia: Eutheria: Primates: Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                   arbitrary Caps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                   be preserved.
                                                                                                                                                                                                                                                                                                                                                                       as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 191887)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insert size: 19500; agarese-tp
Insert size: 189187; sum-of-condigs
Quality enverage: 11.7 in 020 bases; agarese-tp
Quality enverage: 12.0 in 020 bases; sum of-condigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Consensus quality: 182931 bases at least Q40 Consensus quality: 187131 bases at least Q30 Consensus quality: 188492 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chemistry: Dye-terminator Hig Dye: 100% of reads Assembly program: Phrap: worston 0.969721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center clone name: 2545_H, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: sequence_submissions/genome.wi.mit.odu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing verter. Plasmid: n/1; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center project name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www-seq wi mit odu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Whitehead Institute/ MIT Center for Senome Research
                                                                                                                   1334 1433: gap of 100 bp
1434 2336: contig of 903 bp in length
                           317<u>6</u> 3275. gap of
                                                                                                                                                                                                                       643 742: dap of
743 1333: cr
                                                               2436: Jap of
                                                                                                                                                                                                               1333: contig of 591 bp in length
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                                                                                                                                                                                                                                                                                       642: contiq of 642 bp in length
of 100 bp
costiq of 759 bp is length
of 100 bp
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17769 17868: gap of
17869 18637, cont
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139802 191887: contin of 51986 bp in locath
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34770 79954: contig of 45185 bp in length
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25454 34669; con
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14932 | 16544 | 1956
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16595 1669<u>4 : gap</u> of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .1974 12073: gap of
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5143 5242; gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9987 9186; gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8362 8461: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6927 7026; gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5909 6008: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4423 4522: gap of
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5243. .f
                                                                                                                                                                                                                                                                                       /note="assembly_fraqment"
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3276. .4422
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8361: contig of 587 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .191887
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| 100 bp
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14831 contig of 700 bp in length
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34669: centia of 9216 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17768: contig of 1074 bp in length
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10729: contig of 613 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25353: contig of 1423 bp in length
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· subid of 1458 bp in length
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counting of 1663 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (03-SEP-1949) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Feb 1, 2002 this segment version replaced gi:17227242.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ttp-decemb.wasbigates-edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           * are represented as runs of N. the order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
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provided by the submittor.
This sequence will be replaced
by the finished sequence as soon as it is available and

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                                                                                                                                                                                                      http://www.sicer.i...k/fr/j.f./_j.b.jics/w.r.pq_this...poste
was generated from part of Eactorial clone ducting of buman
chromosome 1%, constructed by the Sasyer Centro Chromosome 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               assembly was confirmed by restriction digest. The following abbreviations are used to associate primary acrossic numbers discuint the feature table with their source databases: Em., EMBL; Sw.; SWISSPROT: TT. TREMBL; Wp.; WORMPEP: Information on the WORMPEP database can be found.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  regions were either double-stranded or sequenced with an alternate chemistry or exceed by high quality data (i.e., phred quality (0); an arrempt was made to regolve all sequencing problems, such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CBIO 18A, UK. E-mail enquiries: humquery@sangor.ac.uk Cione requests: cloherequest@sangor.ac.uk
On oct 25, 2001 this sequence version replaced 4i:16214633.
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     Direct Submission

Sabulted (07 SER 2000) Sabact Contro, Blacton, Cambridgeshire,
OB10 186, USE. E mail coglities, bunquotytsasteria.ich Clone
requests: clonerequest@sangeriac.uk
ob Sep 5 (500) rije sessense.
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The true right end of clone RP11-694F24 is at 70148 in this sequence. The true right end of clone RP11-789G22 is at 2000 in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cicac "RFT]-694F24"
/cione_tib="RPCI-11.3"
19535 m 15215 c 15251 m 201
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/dh_+++ "(=von.9006"

/chromosome="13"
Contractive section to the contraction
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Prod. NO. 8.48-55;
C. Mismatthes 102, Indels 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Group. Further information can be found at http://www.senerr.ec.ab.937/hos
http://www.senerr.ec.ab.937/hos
RPI1-549024 is tram the library RPGI-11.2 constructed at the
Roswell Park Cancer Institute by the group of Pleter de Jong. For
further details see http://baspac.aed.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.simer.prok/Projects/T_clejuns.wempog_this sequence-
was generated from part of bacterial clone contigs of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The following abbreviations as used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw.; SW.88SPROF: Tr.; IPEMBL; WP:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence has been finished according to sequence map criteria as Follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     During sequence assembly data is compared from overlapping clones, where differences are found these are annotated as variations
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                                                                                                                                                                                                                                                                                                                                             8303
/note "LIMB7 repeat: matches 5855. .6060 of consensus"
                                                   10859.
                                                                                                                      /note "AhuJb repeat: matches 85, .300 of consensus" complement(9457, .9638)
                                                                                                                                                                                                                                                                       /noio-"ilME repeat: matches 449, ,759 of consensus"
8712, ,8928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note "match: GSS: Em:AQ788293" 6548. .6686
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1. .185467
                                                                                 /note-"AluSx repeat: matches 6, .307 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /noto "LLMA repeat: matches 5236. .5784 of consensus" 6715. .7283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"AluJo repeat: matches 1. .287 of consensus" 2200. .4375
                                                                                                                                                                                                                                                                                                                                                                           /note "FLAM_A repeat: matches 2. .141 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="LIMEd repeat: matches 1066, .1462 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note "AluSx repeat: matches 1. .298 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thete "[110A7 repeats matches Ref? [614] of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       facts "AlaJo repeat. matches 57. .304 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /r.lano . "PP11 - 549D2 3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "I]MPo repeat: watches 1462 2061 of consensus"
                                                                                                                                                                                                                                                                                                                                             . 8588
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/hote "Aluax repeat: matches i...ili of consensus"

15065...15567

/hote "L2 repeat: matches 1810...2355 of consensus"
  /note-"AluJo répeal: matches l. .255 of consensus"
37167. .37248
                                               /note "L2 repeat: matches 2653, .2705 of consensus" 36738, .37033
                                                                                                                                         /note-"AluJb repeat: matches 6.
35394. .35445
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="L1ME3A repeat: matches 5797, .5932 of consensus" \$1704 , .32012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"L1MB5 repeat: matches 5974, .5865 of consensus" 
31960, .31703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"AluJb repeat: matches 1, .298 of conscisus"
28039, .28978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mote-"Alulb repeat: matches 1. .312 of consensus" 28131. .28418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="match: STS: Em:AF191952"
27348, .27648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="match: STS: Em:AF191939"
27143. .27812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"FRAN repeat. matches 9, .163 of consensus complement(26457, .27119)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25084. .25216
/hote: "12 repeat matches 2579. .2710 of consensus"
25749_.25903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="AluJb repeat: matches 2. .292 of consensus" 23730. .23903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mote="MIR repeat: matches 155
22821. .23119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /hote-"AluSx repeat: matches l. .497 of consensus"
21264. .21560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (19574
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17630, .17991
/note-"match: CSS: Em:B38273"
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/mote "AluSx repeat: matches !.
complement(15863. .16438)
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/hote "Alusx repeat: matches 1...294 of consensus"
                                                                                                                 /note-"MIR repeat: matches 161. .250 of conscusus"
                                                                                                                                                                                        34854
                                                                                                                                                                                                           /note-"MIR repeat: matches 196.
                                                                                                                                                                                                                                                        /note-"AluSx repeat; matches 25. .304 of consensus"
                                                                                                                                                                                                                                                                                /note="AluSx repeat: matches 218, .248 of consensus"
3416] 34432
                                                                                                                                                                                                                                                                                                                            33018.
                                                                                                                                                                                                                                                                                                                                                                                                                                     /note "AluSx repeat: matches 1, .312 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"Alusx repeat, matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /inster"Alujo repeat: Matches L. 1287 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="AluSx repeat: matches l. .304 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="29 copies 2 mer qa 69% conserved"
complement(17204. .17559)
                                                                                                                                                                                                                                                                                                                                                                                        Juose "LIMERA repeat, matches [428, 1579] of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                    32013.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="THE1B repeat: matches l. .364 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="AluJb repeat: matches l. .297 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="LIMD1 repeat: matches 5712, .5886 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18647
                                                                                                                                                                                                                                                                                                                                             "note-"AluSa repeat. Matches 1. .250 of consensus"
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42562    .42967
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45940, .46252
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19204, .40502
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                                                                                                                                                     Direct Submission

Submitted (07 NeW 2001) Department of Genetics, Washington
Submitted (04 NeW 2001) Lepartment of Genetics, Missouri 64108, USA
Third 24, 2001 this sequence versitation laborated filts20291.
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                       Contact: sapiens@watson.wustl.edu
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NOTICE. This sequence may now represent the ending sequence overlapping clone. It may be shorter because we only sequence overlapping clone sections are provided a small over This sequence may not represent the entire insert of this

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 40); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was continued by restriction digest.

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MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. Mepherson, Department of Genetics, Washington University, St. Louis Ms. For additional information about the map position of this sequence, see bitp://prosmorws.ii.edu.

SOURCE INFORMATION:

donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E., Tateno,M., Catanese,J.J. and de Jong,P.J. (1988) An improved approach for construction of bacterial artificial chromosome libraries. Genemics 51:18. The close may be obtained either from bessearch shell is. In . (http://www.rossen.com/ or Pieter de Jong and esweckers at the Meswell Park Cancer Institute The RPCI-11 human BAC library was made from the blood of one male

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VECTOR: pBACe3.6
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13129.
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18642.
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14668. .14755
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//dh_stet "taxob.5606"

/chromosome-"2"
                             /rpt_tamily."MalR"
25519. .25816
                                                                             /rpt_family="AI_rich"
24243, .24487
     25904. . 25966
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14387. .14667
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Query Match 8.0%; Score 227.4; DB 9; Length 144455; Best Local Similarity 80.2%; Pred. No. 1.2e+54; Matches 267, Conservative 0; Mismatches 66; Indels 0; Gape
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46279. .4
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45358. .4
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47176. .48678
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43211, .43510
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41151. .418
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39413. .39589
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38264.
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26064. .26379
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39025. .39244
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38545. .38585
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37756. .38061
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37537. .37566
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35170. .36476
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14633. .45357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Consensus quality: 156088 bases at least 040 consensus quality: 162568 bases at least 020 consensus quality: 163599 bases at least 020 Estimated insert size: 16000, sum-of-contigs estimation Estimated insert size: 160034, sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Setweithed (05 AFP 2000) Preductive Sequencing Prility, ESECTION Genome Institute, 2800 Mitchell Drive, Walnut Greek, CA 94598, USA ON 19 19 2000 this segronce service replaced F19655958.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases I to 166534)
DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * NOTE: This is a 'working draft' sequence if currently 
* consists of 12 contigs. Gaps between the contigs 
* are represented as runs of N. The order of the pieces 
* its believed to be correct as given, however the sizes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality coverage: 8.94 in Q20 bases; pulse field get estimation Quality coverage: 9.1 in Q20 bases; sum-of-contids estimation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Summary Statistics
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Center Code:
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Mammalia: Puthoria: Primatos: Cuturchini: mominidae: Domo
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                                                                                                                                                                                                                                                                                                                                                                                                          of the gaps between them are based on estimates that have provided by the submittor. This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                              the accession number will be preserved.

1 3977: contig of 3077 by in length
                                                                                                                                                                                                                                                                                                                                                                                       by the finished sequence as soon as it is available and
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41849
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74236
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107151: gap of mnknown length
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58536:
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                   dap of unknown length contig of 18361 bp in length
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contig of 2538 bp in length
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contig of 16077 bp in length
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                                                            AUTHOKS
TITLE
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Shimizu,N. and Asakawa,S.
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